

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2003, 14:38:21 : Search time 2327 Seconds  
(without alignments)  
12527.665 Million cell updates/sec

Title: US-09-319-724A-13  
Perfect score: 1800  
Sequence: 1 ccgcgcgcgtgctgctg.....gtggaacttgcacagcaaaa 1800

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estmu:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_hic:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_hic:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: gb\_gss:\*
  - 18: em\_gss\_hum:\*
  - 19: em\_gss\_inv:\*
  - 20: em\_gss\_pln:\*
  - 21: em\_gss\_vrt:\*
  - 22: em\_gss\_fun:\*
  - 23: em\_gss\_mam:\*
  - 24: em\_gss\_mus:\*
  - 25: em\_gss\_Other:\*
  - 26: em\_gss\_pro:\*
  - 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	812.6	45.1	879	14	BQ437992
2	793.2	44.1	1098	13	BM554832
3	734.4	40.8	1121	13	BM466309
4	707.6	39.3	1046	13	BM462090
5	693.6	38.5	744	12	BF732416
6	683.8	38.0	976	14	BM804893

7	663.6	36.9	700	12	BF110352
8	663.2	36.8	682	12	BF445098
9	655.4	36.4	749	9	AI317419
10	653.4	36.3	663	12	BF062374
11	652.2	36.2	699	12	BG252894
12	648.8	36.0	693	12	BG499066
13	642.8	35.7	748	13	BI089285
14	634.8	35.3	752	10	AW475143
15	618.4	34.4	772	12	BG252656
16	614.4	34.1	619	10	AW576585
17	613.8	34.1	714	10	AW475466
18	610	33.9	918	12	BG287562
19	601.2	33.4	670	12	BG621630
20	598	33.2	939	14	BQ958528
21	590.2	32.8	971	12	BG171028
22	583.4	32.4	608	12	BF941584
23	583	32.4	616	14	BQ638442
24	581.2	32.3	721	12	BE868698
25	578	32.1	684	12	BE848488
26	577.6	32.1	601	10	AW305358
27	576.4	32.0	912	12	BE905485
28	575.4	32.0	662	9	AI172333
29	567.8	31.5	731	13	BI868308
30	564.4	31.4	566	14	BM827392
31	563.4	31.3	610	10	AW263003
32	559.4	31.1	574	12	BG492937
33	559.4	31.1	693	9	AA057428
34	558	31.0	587	12	BF434917
35	551.6	30.6	848	12	BG244043
36	548.8	30.5	681	12	BF105260
37	546.4	30.4	709	9	AA800019
38	545.2	30.3	769	12	BG619729
39	542	30.1	547	12	BG718166
40	538.2	29.9	903	14	BQ233844
41	536	29.8	552	9	AL550770
42	535.4	29.7	926	12	BE872774
43	534.6	29.7	959	12	BF447674
44	534.6	29.7	852	12	BF181943
45	531.6	29.5	960	13	BI852732

ALIGNMENTS

RESULT 1  
LOCUS BQ437992 879 bp mRNA linear EST 24-MAY-2002  
DEFINITION AGENCOURT\_7894720 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6158457  
5', mRNA sequence.  
ACCESSION BQ437992  
VERSION BQ437992.1 GI:21177068  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 879)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.  
cDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: L14M13505 row: p column: 10  
High quality sequence stop: 627.  
Location/Qualifiers 1. .879

FEATURES  
source

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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."
BASE COUNT      220 a 152 c 200 g 306 t 1 others
ORIGIN

Query Match      45.1%; Score 812.6; DB 14; Length 879;
Best Local Similarity 98.1%; Pred. No. 1.3e-188;
Matches 843; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Qy 678 TTAGTTTCAATGATTTAATGAGAACATTAAGAAAGATTATGCTCGGTACAGTAAAGAG 737
Db 1 TTAGTTTCAATGATTTAATGAGAACATTAAGAAAGAA-TATGCTCGGTACAGTAAAGAG 59

Qy 738 GAAGAAATGGATGATATGGATAGAGACCTAGGAGATGAATATGATGGAACAGGTGCAT 797
Db 60 GAAGAAATGGATGATATGGATAGAGACCTAGGAGATGAATATGATGGAACAGGTGCAT 119

Qy 798 GGAGATGATTTAGACCATCAAGTCACCCACTGATATTTCTCTCTCTCTGATTTGGTCTGGA 857
Db 120 GGAGATGATTTAGACCATCAAGTCACCCACTGATATTTCTCTCTCTCTGATTTGGTCTGGA 179

Qy 858 TGTCAGATATTTGCTGTCTCTCATCGTTATATATGTTGCAATGATAGAGATTATAT 917
Db 180 TGTCAGATATTTGCTGTCTCTCATCGTTATATATGTTGCAATGATAGAGATTATAT 239

Qy 918 ACTGAGAGGGATCAATGCTCAGTACAGCCATATTTGCTATGCTGCTACCTCTCCAGTG 977
Db 240 ACTGAGAGGGATCAATGCTCAGTACAGCCATATTTGCTATGCTGCTACCTCTCCAGTG 299

Qy 978 AATGGTTATTTGGAGGAAGTCTGTATGCTAGACAAGGAGGAGAGATGATGAAGAGAG 1037
Db 300 AATGGTTATTTGGAGGAAGTCTGTATGCTAGACAAGGAGGAGAGATGATGAAGAGAG 359

Qy 1038 ATGTTTATGGGGGATTCCTTATCCAGCTATGTTGTTGGCACTGCTCTTCATCAAT 1097
Db 360 ATGTTTATGGGGGATTCCTTATCCAGCTATGTTGTTGGCACTGCTCTTCATCAAT 419

Qy 1098 TTCATAGCCATTTATACCATGCTTCAAGAGCCATTCCTTTTGGACAATGGTGGCCGTT 1157
Db 420 TTCATAGCCATTTATACCATGCTTCAAGAGCCATTCCTTTTGGACAATGGTGGCCGTT 479

Qy 1158 TGTTGCATCTCTTTTGTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1217
Db 480 TGTTGCATCTCTTTTGTATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 539

Qy 1218 AATCTGCAGTCAGCCCAACTTCTTCTGTCGTCTCAATGCTGCTCCCTGCTCTATACCG 1277
Db 540 AATCTGCAGTCAGCCCAACTTCTTCTGTCGTCTCAATGCTGCTCCCTGCTCTATACCG 599

Qy 1278 GAGAAAAATGGTTCATGGAGCCCTGGGTTATCTTTGCTGGTGGTGGTGGTGGTGGTGGTGG 1337
Db 600 GAGAAAAATGGTTCATGGAGCCCTGGGTTATCTTTGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 659

Qy 1338 GGTTCATCTTTTATTTGAATGATTTTATCTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 1397
Db 660 GGTTCATCTTTTATTTGAATGATTTTATCTCTTCACTCTCTCTCTCTCTCTCTCTCTCTCTCT 719

Qy 1398 TATGCTATGCTTCATGATGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1457
Db 720 TATGCTATGCTTCATGATGCTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 779

Qy 1458 ACTATTGTGTCACATATTTTCTACTAAATCGAGAAGATTACCGG-TGGCAATGCAAG 1516
Db 780 ACTATTGTGTCACATATTTTCTACTAAATCGAGAAGATTACAGGTGGCAANTGGACAA 839

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/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: small intestine; Vector: pCMV-SPORT6;
Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally;
Oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
BASE COUNT      286 a 190 c 258 g 364 t
ORIGIN

Query Match      44.1%; Score 793.2; DB 13; Length 1098;
Best Local Similarity 98.5%; Pred. No. 7.6e-184;
Matches 843; Conservative 0; Mismatches 8; Indels 5; Gaps 4;

Qy 505 TGAACCTGGTTCCAAATCTAAATCCAGATGTCATATTCAGTAAATGGAAGAAAGTCAG 564
Db 1 TGAACCTGGTTCCAAATCTAAATCCAGATGTCATATTCAGTAAATGGAAGAAAGTCAG 60

Qy 565 ATGTGAAATTTGAAGATCGATTTGACAAATATCTTGATCGTCCCTTTTCAACATCGGA 624
Db 61 ATGTGAAATTTGAAGATCGATTTGAC-AAATCTTGATCGTCCCTTTTCAACATCGGA 119

Qy 625 TTCATTGGTTTTCAAATTTTCAACTCTTCATGATGGTGCATCTTCTTGGTGGGCTTAGTTT 684
Db 120 TTCATTGGTTTTCAAATTTTCAACTCTTCATGATGGTGCATCTTCTTGGTGGGCTTAGTTT 179

Qy 685 CAATGATTTTAATGAGAACATTAAGAAAGATTAATGCTCGGTACAGTAAAGAGAGAGAAA 744
Db 180 CAATGATTTTAATGAGAACATTAAGAAAGATTAATGCTCGGTACAGTAAAGAGAGAGAAA 239

Qy 745 TGGATGATATGGATAGACCTAGGAGATGAATATGATGGAACAGCTGCATGGAGATG 804
Db 240 TGGATGATATGGATAGACCTAGGAGATGAATATGATGGAACAGCTGCATGGAGATG 299

Qy 805 TATTTAGACCATCAAGTACCCACTGATATTTTCCCTCTCTCTGATTTGTTGGTGTGATGTCAGA 864
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LOCUS	BM462090	1046 bp	mRNA	linear	EST 05-FEB-2009
DEFINITION	AGENCOURT_6424576 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5491167 5', mRNA sequence.				
ACCESSION	BM462090				
VERSION	BM462090.1 GI:18511130				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1046)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: egapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM12111 row: d column: 16 High quality sequence stop: 574.				
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	/lab_host="DH10B (phage-resistant)"				
	/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."				
BASE COUNT	272 a	209 c	205 g	360 t	
ORIGIN					
Query Match	39.38; Score 707.6; DB 13; Length 1046;				
Best Local Similarity	99.3%; Pred. No. 7.6e-163;				
Matches	721; Conservative	0; Mismatches	4; Indels	1; Gaps	1;
Qy	1076	TGGCAGCTGCCCTTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAGCAATTC	1135		
Db	1	TGGCAGCTGCCCTTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAGCAATTC	60		
Qy	1136	TTTTGGACAATGGTGGCGGTGTTGCATCTGTTTTTTTGTATTCTCTCTCAAATCT	1195		
Db	61	TTTTGGACAATGGTGGCGGATGTGTCATCTGTTTTTTTGTATTCTCTCTCAAATCT	120		
Qy	1196	TGTTGGTACAATACTTGGCCGAAATCTGTCAAGTCAGGCCAACCTTTCCTTGTGCGTGCAA	1255		
Db	121	TGTTGGTACATACTTGGCCGAAATCTGTCAAGTCAGGCCAACCTTTCCTTGTGCGTGCAA	180		
Qy	1256	TGCTGTGCCTCGTCCCTATACCGGAGAAAAATGGTTCATGAGAGCGCTGGGTTATGTTTG	1315		
Db	181	TGCTGTGCCTCGTCCCTATACCGGAGAAAAATGGCTCATGGAGCGCTGGGTTATGTTTG	240		
Qy	1316	CCTGGTGGAAATTTACCTTTTGTTCAATCTTATTGAATGATTTATTCATCTTCACGTC	1375		
Db	241	CCTGGTGGAAATTTACCTTTTGTTCAATCTTATTGAATGATTTATTCATCTTCACGTC	300		
Qy	1376	TTTCTGGGCATATAGATCTATTATGTCATGGCTTCATGATGCTGGTGCCTGGTTATCCT	1435		
Db	301	TTTCTGGGCATATAGATCTATTATGTCATGGCTTCATGATGCTGGTGCCTGGTTATCCT	360		
Qy	1436	GTGCAATTGTGACTGTCTGTGACATATTGTGTGCACATATTTTCTACAAATGCGAAGA	1495		
Db	361	GTGCAATTGTGACTGTCTGTGACATATTGTGTGCACATATTTTCTACTAAATGCAGAGA	420		
Qy	1496	TTACCGGTGGCAATGGACAAGCTTTTCTCTCGCTGCATCAACTGCAATCTATGTTACAT	1555		



[illegible]

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Invitrogen  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12716 row: m column: 07  
High quality sequence stop: 626.  
Location/Qualifiers  
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;  
Site1: EcoRV (destroyed); Site2: NotI; RNA source pool  
of three ovaries, from females ranging in age from 38 to  
49 yo. Library is oligo-dT primed and directionally cloned  
(EcoRV site is destroyed upon cloning). Average insert  
size 2.1 kb, insert size range 1-3.5 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics

BASE COUNT	236	a	208	c	211	g	321	t	
ORIGIN	Clicking CODE 030.								
Query Match	38.0%; Score 683.8; DB 14; Length 976;								
Best Local Similarity	97.3%; Pred. No. 5.3e-157;								
Matches	727;	Conservative	0;	Mismatches	17;	Indels	3;	Gaps	3;
Qy	928	GATCAATGCTCAGTACAGCCATATTTGCTATGCTGTACGCTCCAGTCAATGGTTATT	987						
Db	1	GATCAATGCTCAGTACAGCCATATTTGCTATGCTGTACGCTCCAGTCAATGGTTATT	60						
Qy	988	TTGGAGGAAGTCTCTATGCTACAGAAGGAGGAGATGGATAAAGCAGATGTTTATTG	1047						
Db	61	TTGGAGGAAGTCTCTATGCTACAGAAGGAGGAGATGGATAAAGCAGATGTTTATTG	120						
Qy	1048	GGGCAATTCCTTATCCCAAGCTATGGTGTGGCACTGCCCTTCTCATCAATTTCAAGCCA	1107						
Db	121	GGGCAATTCCTTATCCCAAGCTATGGTGTGGCACTGCCCTTCTCATCAATTTCAAGCCA	180						
Qy	1108	TTTATTACCATGCTTCAAGAGCCATTCCTTTTGAAACAAATGGTCGGCTTTGTTGCAATCT	1167						
Db	181	TTTATTACCATGCTTCAAGAGCCATTCCTTTTGAAACAAATGGTCGGCTTTGTTGCAATCT	240						
Qy	1168	GTTTTTTTGGTTATTTCCTCTAAATCTGTTGGTACAAATCTTTGGCCGAAATCTGTGAG	1227						
Db	241	GTTTTTTTGGTTATTTCCTCTAAATCTGTTGGTACAAATCTTTGGCCGAAATCTGTGAG	300						
Qy	1228	GTGAGCCCAACTTTCCTTGTCGTGTCAAATGCTGTGCCCTGCTCTATACCGGAGAAAAAT	1287						
Db	301	GTGAGCCCAACTTTCCTTGTCGTGTCAAATGCTGTGCCCTGCTCTATACCGGAGAAAAAT	360						
Qy	1288	GGTTTCATGGAGCCGCGGTTATTCTTTTGCCCTGGCTGGAATTTTACCCTTTGGTTCAATCT	1347						
Db	361	GGTTTCATGGAGCCGCGGTTATTCTTTTGCCCTGGCTGGAATTTTACCCTTTGGTTCAATCT	420						
Qy	1348	TTATTGAAATGATTTTCATCTTCACGCTTTTCTGGGCATATAAGATCTATATGCTCATG	1407						
Db	421	TTATTGAAATGATTTTCATCTTCACGCTTTTCTGGGCATATAAGATCTATATGCTCATG	480						
Qy	1408	GCTTCATGATGCTGCTGCTGGTTATCTCTGTCATTTGTCACCTGCTGTGTGACTATTGTGT	1467						
Db	481	GCTTCATGATGCTGCTGCTGGTTATCTCTGTCATTTGTCACCTGCTGTGTGACTATTGTGT	540						
Qy	1468	GCACATATTTTCTACTAAATGCAGAAATTTACCGGTGGCAATGGACAAGTTTTCCTCTCTG	1527						







D	b	661	GCC	663
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<p>Db 301 CATATAAGATCTATTATGTCCTATGGCTTGCATGATCGTGCTGGTTATCCTGTGCATTTG 360</p> <p>Qy 1444 TGACTGTCTGTGCACTATTGTCGTGCACATATTTTTCTAAATGACAAGATTACCCTG 1503      </p> <p>Db 361 TGACTGTCTGTGCACTATTGTCGTGCACATATTTTTCTAAATGACAAGATTACCCTG 420      </p> <p>Qy 1504 GCAATGGAAGAAGTTTCTCTGTCGTCATCAACTGCAATCTATGTTTACATGTAATTCCT 1563      </p> <p>Db 421 GGCAATGGAAGAAGTTTCTCTCTGTCGTCATCAACTGCAATCTATGTTTACATGTAATTCCT 480      </p> <p>Qy 1564 TTACTACTATTTTTCAAACAAGAAGATGATGGCTTATTTCAAACATCATTTTACTTTG 1623      </p> <p>Db 481 TTTACTACTATTTTTCAAACAAGAAGATGATGGCTTATTTCAAACATCATTTTACTTTG 540      </p> <p>Qy 1624 GATATATGCGGGTATTAGCACAGCCTTGGGATATGTCGGAGCGATTGGTTACATGG 1683      </p> <p>Db 541 GATATATGCGGGTATTAGCACAGCCTTGGGATATGTCGGAGCGA-TGGTTACATGG 599      </p> <p>Qy 1584 GAACAAGTGCCTTTGCCG--AAAAATCTATCTACTATGTAATAATTTGACTAGAACCCAA 1741      </p> <p>Db 600 GACAAGTGCCTTTGCCGCAAAAATCTATACTAATGTCACATTTGACTAGAGAACAA 659      </p> <p>Qy 1742 GAAACCTGGAACCTTTGGATCAATTTCTTTTCATAGGG 1780      </p> <p>Db 660 GAAACCTGGAACCTTTGGATCAATTTCTTTTCATAGGG 698      </p>				
<hr/>				
<p>RESULT 12</p> <p>LOCUS BG499066</p> <p>DEFINITION 602545458F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4667846 5', mRNA linear EST 27-MAR-2001</p> <p>ACCESSION BG499066</p> <p>VERSION BG499066.1 GI:13460583</p> <p>KEYWORDS EST.</p> <p>SOURCE human.</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>REFERENCE 1 (bases 1 to 693)</p> <p>AUTHORS NTH-MGC http://mgc.nci.nih.gov/</p> <p>TITLE National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p>JOURNAL Unpublished (1999)</p> <p>COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: DCTD/DMP CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1477 row: c column: 15 High quality sequence stop: 693.</p>				
<hr/>				
<p>FEATURES</p> <p>source</p> <p>1..693</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone_lib="NIH_MGC_60"</p> <p>/tissue_type="adenocarcinoma"</p> <p>/lab_host="DH10B (T1 phage-resistant)"</p> <p>/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SflI (ggccgcctcgcc); Site_2: SfiI (ggccattatggcc) ; Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCATTTATGGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGGCATG-dp(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC</p>				
<hr/>				
<p>Query Match 36.2%; Score 652.2; DB 12; Length 699;</p> <p>Best Local Similarity 97.7%; Pred. No. 2.9e-149;</p> <p>Matches 683; Conservative 0; Mismatches 13; Indels 3; Gaps 2;</p>				
<hr/>				
<p>Qy 1084 CCTCTTCATCAATTTTCATAGCCATTTATTACCATCCTTCAAGAGCCATTCCTTTGGAA 1143      </p> <p>Db 1 CCTCTTCATCAATTTTCATAGCCATTTATTACCATCCTTCAAGAGCCATTCCTTTGGAA 60      </p> <p>Qy 1144 CAATGGTGGCGTTGTTGCATCTGTTTTTTGTTATTCCTCTCAATCTGTTGGTA 1203      </p> <p>Db 61 CAATGGTGGCGTTGTTGCATCTGTTTTTTGTTATTCCTCTCAATCTGTTGGTA 120      </p> <p>Qy 1204 CAATACCTTGGCGGAATCTCTCAGGTACGCCCAACTTTCCTTGTGCTGTCATGCTGTGC 1263      </p> <p>Db 121 CAATACCTTGGCGGAATCTCTCAGGTACGCCCAACTTTCCTTGTGCTGTCATGCTGTGC 180      </p> <p>Qy 1264 CTCCTCTCTATACCGGAGAAAAATGTCATGAGCGCTCGGTTATTTGTTCCCTGGTG 1323      </p> <p>Db 181 CTCCTCTCTATACCGGAGAAAAATGTTTCATGGAGCGCTCGGTTATTTGTTCCCTGGTG 240      </p> <p>Qy 1324 GAATTTTACCTTTTGGTTCAATCTTTATTTGAATGATTTATCTTCAGCTCTTTCTCGG 1383      </p> <p>Db 241 GAATTTTACCTTTTGGTTCAATCTTTATTTGAATGATTTATCTTCAGCTCTTTCTCGG 300      </p> <p>Qy 1384 CATATAAGATCTATTATGTCCTATGGCTTCATGATGCTGCTGCTGTTATCCTGTGCATTTG 1443      </p>				
<hr/>				
<p>Db 661 GCC 663</p> <p>   </p> <p>RESULT 11</p> <p>LOCUS BG252894</p> <p>DEFINITION 602365488F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4473861 5', mRNA linear EST 13-FEB-2001</p> <p>ACCESSION BG252894</p> <p>VERSION BG252894.1 GI:12762710</p> <p>KEYWORDS EST.</p> <p>SOURCE human.</p> <p>ORGANISM Homo sapiens</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>REFERENCE 1 (bases 1 to 699)</p> <p>AUTHORS NTH-MGC http://mgc.nci.nih.gov/</p> <p>TITLE National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p>JOURNAL Unpublished (1999)</p> <p>COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-re@mail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM10296 row: p column: 22 High quality sequence stop: 697.</p>				
<hr/>				
<p>FEATURES</p> <p>source</p> <p>1..699</p> <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone_lib="NIH_MGC_90"</p> <p>/tissue_type="adenocarcinoma, cell line"</p> <p>/lab_host="DH10B (phage-resistant)"</p> <p>/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 Kb. Library enriched for full-length clones and constructed by Life technologies. Note: this is a NIH_MGC Library."</p> <p>BASE COUNT 168 a 133 c 140 g 258 t</p> <p>ORIGIN</p>				







DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10298 row: j column: 03  
High quality sequence stop: 702.  
Location/Qualifiers  
1. .772  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4474466"  
/clone\_lib="NIH\_MGC\_90"  
/tissue\_type="adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site:1: NotI;  
Site:2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 Kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."  
BASE COUNT 186 a 144 c 164 g 278 t  
ORIGIN

Query Match 34.4%; Score 618.4; DB 12; Length 772;  
Best Local Similarity 95.8%; Pred. No. 5.8e-141;  
Matches 711; Conservative 0; Mismatches 21; Indels 10; Gaps 7;  
QY 1049 GGCATTCCCTATCCAGCTATGGTGTGGCACTGCTTCTTCATCAATTCATAGCCAT 1108  
Db 1 GGCATTCCCTATCCAGCTATGGTGTGGCACTGCTTCTTCATCAATTCATAGCCAT 60  
QY 1109 TTATTACCATGCTTCAAGAGCCATTCCCTTTTGGACAATGGTGGCCGTTTGTGCATCTG 1168  
Db 61 TTATTACCATGCTTCAAGAGCCATTCCCTTTTGGACAATGGTGGCCGTTTGTGCATCTG 120  
QY 1169 TTTTGTGTTTATTCCTCCTAAATCTTGTGTGTAATACCTTGGCCGAAATCTGTGAGG 1228  
Db 121 TTTTGTGTTTATTCCTCCTAAATCTTGTGTGTAATACCTTGGCCGAAATCTGTGAGG 180  
QY 1229 TCAGCCCAACTTTCCCTGTGCTCAATGCTGCTGCTGCTATACCGGAGAGAAAAATG 1288  
Db 181 TCAGCCCAACTTTCCCTGTGCTCAATGCTGCTGCTGCTATACCGGAGAGAAAAATG 240  
QY 1289 GTTCATGGAGCCTGCGGTTATTGTTTGCCTGGGTGGAATTTTACCTTTTGGTTCAATCTT 1348  
Db 241 GTTCATGGAGCCTGCGGTTATTGTTTGCCTGGGTGGAATTTTACCTTTTGGTTCAATCTT 300  
QY 1349 TATTGAATGTAATTCATCTTCACGTCTTTCGCGCATATAGATCTATATGCTCTATGG 1408  
Db 301 TATTGAATGTAATTCATCTTCACGTCTTTCGCGCATATAGATCTATATGCTCTATGG 360  
QY 1409 CTTTCATGATGCTGCTGCTGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1468  
Db 361 CTTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420  
QY 1469 CACATATTTTCTACTAAATCCAGAGATTACCGGTGGCAATGGACAAGTTTCTCTCTGC 1528  
Db 421 CACATATTTTCTACTAAATCCAGAGATTACCGGTGGCAATGGACAAGTTTCTCTCTGC- 479  
QY 1529 TGCATCACTGCAATCTATGTTTACATGATATTCCTTTTACTACTATTTTTCAAAAACAA 1588  
Db 480 TGCATCACTGCAATCTATGTTTACATGATATTCCTTTTACTACTATTTTTCAAAA-AAA 538  
QY 1589 GATGATATGCTTATTTCAACATCATTTTACTTTGGATATATGGCGGTATTTAGCACAGC 1648  
Db 539 GATGATAGG-TTATTTCAACATCATTTTACTTTGGATATATGGCGGTATTTAGCACAG- 596  
QY 1649 CTTGGGGATAATGTGGAGCGATTGGTTTACATGGGAACAGTGCCTTTGTCGGAATAAT 1708  
Db 597 CTTGGGGATAATGTGGAGCGATTGGTTTACCTGGGAACA---GTGCTTTTGTGGAATAAA 653  
QY 1709 CTATACTAATGCAAAATTCAGTAGAGACCCCAAGAAACCTGGAACCTTTGGATCAATTC 1768  
Db 654 TTATCTAATGTGAAA--TTGATAGAGAACCAAGAAACCTGGGAACCTTTGGATTCATTC 711

QY 1769 TTTTTCATAGGGGTGGAACCTTG 1790  
Db 712 -TTTTCATACGGGTGGAACCTTG 732  
Search completed: January 20, 2003, 16:29:38  
Job time : 2344 secs



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Db	133	AAGTACTTTTCACTTCCTGTTGGGCTCAAAAAAGTATCAGTCAATTACCATGAA	192
QY	198	ACTCTGGGAGAACACTTCAAGGGGTGAATTTAGTGGTCTGGATATTAATTTT	257
Db	193	ACTCTGGGAGAACACTTCAAGGGGTGAATTTAGTGGTCTGGATATTAATTTT	252
QY	258	AAAGATGATGTGATGCCAGCCACTTACTGTGAATTTGATTTAGATAAAGAAAGAGAT	317
Db	253	AAAGATGATGTGATGCCAGCCACTTACTGTGAATTTGATTTAGATAAAGAAAGAGAT	312
QY	318	GCATTTGTATATGCCATAAAAAATCATTTACTGTACCAGATGTACATAGATGATTTACCA	377
Db	313	GCATTTGTATATGCCATAAAAAATCATTTACTGTACCAGATGTACATAGATGATTTACCA	372
QY	378	ATATGGGGTATTTGGTGGAGGCTGATGAAATGGAGAAGATTTACTCTTTGGACCTAT	437
Db	373	ATATGGGGTATTTGGTGGAGGCTGATGAAATGGAGAAGATTTACTCTTTGGACCTAT	432
QY	438	AAAAAACTTGAATAGTGTAAATGAATCGAATTTGTTGATGTTAACTTAAGTACTGAA	497
Db	433	AAAAAACTTGAATAGTGTAAATGAATCGAATTTGTTGATGTTAACTTAAGTACTGAA	492
QY	498	GGAAGGTGAAACTGGTTCCAAATACTAAATCCAGATGTCAATTTACAGTAAATGGAA	557
Db	493	GGAAGGTGAAACTGGTTCCAAATACTAAATCCAGATGTCAATTTACAGTAAATGGAA	552
QY	558	AAGTCAGATGTGAATTTGAAGATCGATTTGACAAATATCTTGATCCGCTCTTTTTCAA	617
Db	553	AAGTCAGATGTGAATTTGAAGATCGATTTGACAAATATCTTGATCCGCTCTTTTTCAA	612
QY	618	CATCGGATCATTTGGTTTTCATTTTCAACTCCTTCAATGATGATGATGATGATGATG	677
Db	613	CATCGGATCATTTGGTTTTCATTTTCAACTCCTTCAATGATGATGATGATGATGATG	672
QY	678	TTAGTTTCAATGATTTTAAATGAGAACATTAAGAAAGATTTATGCTCGGTACAGTAAGAG	737
Db	673	TTAGTTTCAATGATTTTAAATGAGAACATTAAGAAAGATTTATGCTCGGTACAGTAAGAG	732
QY	738	GAAGAAATGGATGATATGATAGACACCTAGGAGATGAATATGGATGGAAACAGGTGCAT	797
Db	733	GAAGAAATGGATGATATGATAGACACCTAGGAGATGAATATGGATGGAAACAGGTGCAT	792
QY	798	GGAGATGTATTTAGACCATCAAGTACCACCTGATATTTTCCCTCTCTGATTTGGTCTGGA	857
Db	793	GGAGATGTATTTAGACCATCAAGTACCACCTGATATTTTCCCTCTCTGATTTGGTCTGGA	852
QY	858	TGTCAGATATTTGCTGTGCTCTCATCGTTATTTATTTGTCATGATGATGATGATGATG	917
Db	853	TGTCAGATATTTGCTGTGCTCTCATCGTTATTTATTTGTCATGATGATGATGATGATG	912
QY	918	ACTGAGAGGGGATCAATGCTCAGTACAGCCATATTTGCTCTATGCTCTAGTCTCAGTIG	977
Db	913	ACTGAGAGGGGATCAATGCTCAGTACAGCCATATTTGCTCTATGCTCTAGTCTCAGTIG	972
QY	978	AATGGTTATTTTGGAGGAAGTCTGATGCTAGACAAGGAGGAGATGGATAAAGCAG	1037
Db	973	AATGGTTATTTTGGAGGAAGTCTGATGCTAGACAAGGAGGAGATGGATAAAGCAG	1032
QY	1038	ATGTTTATTTGGGGCATTTCTTATCCAGCTATGGTGTGGCACTGCCCTTCTTCATCAAT	1097
Db	1033	ATGTTTATTTGGGGCATTTCTTATCCAGCTATGGTGTGGCACTGCCCTTCTTCATCAAT	1092
QY	1098	TTTCATAGCCATTTATTTACCATGCTTCAAGAGCATTTCTTTTGGAAACAATGGTGGCGTT	1157
Db	1093	TTTCATAGCCATTTATTTACCATGCTTCAAGAGCATTTCTTTTGGAAACAATGGTGGCGTT	1152
QY	1158	TGTTGGATCTGTTTTTGTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1217
Db	1153	TGTTGGATCTGTTTTTGTGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1212
QY	1218	AATCTCTCAGGTACGCCCAACTTTTCCCTGCTGTGTCATGCTGTGCTCTCTCTCTCTCT	1277

Db	1213	AATCTCTCAGGTACGCCCAACTTTTCTTGTGCTGTCAATGCTGTGCTCTCTCTATACCG	1272
QY	1278	GAGAAAAATGGTTTCATGGAGCCTGGGTTATTTGTTGCTGGTGGAAATTTTACCTTTT	1337
Db	1273	GAGAAAAATGGTTTCATGGAGCCTGGGTTATTTGTTGCTGGTGGAAATTTTACCTTTT	1332
QY	1338	GGTTCAATCTTTATTTCAAAATGATTTTCACTTCCACGCTCTTTCTGGGCATATAAGATCTAT	1397
Db	1333	GGTTCAATCTTTATTTCAAAATGATTTTCACTTCCACGCTCTTTCTGGGCATATAAGATCTAT	1392
QY	1398	TATGCTCTATGGCTTCATGATGCTGGTGGTTATCTCTGTCATTTGTCATGTCGTGTG	1457
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QY	1458	ACTATTTGTGTGCACATATTTTCTACTAAATGCAGAGATTTACCGTGGCAATGGCAAGT	1517
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QY	1518	TTTCTCTCTGCTGCATCAACTGCAATCTATGTTTACATGATGATTTCTTTACTACTATTTT	1577
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QY	1578	TTCAAAACAAAGATGTATGGCTTTATTTCAAAACATCATTTTACTTTTGGATATATGGCGTA	1637
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QY	1638	TTTAGACAGAGCCTTGGGGATAATGCTGTGGAGCGATTTGGTTACATGGAGCAAGTGGCTTT	1697
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QY	1698	GTCCGAAAAATCTATACTAATGTGAAAAATTTGACTAGAGACCCCAAGAAAAACCTGGAACCTTT	1757
Db	1693	GTCCGAAAAATCTATACTAATGTGAAAAATTTGACTAGAGACCCCAAGAAAAACCTGGAACCTTT	1752
QY	1758	GGATCAATTTCTTTTTCATAGGGGTGGAACCTTGCACAGCAAAA	1800
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RESULT 2

US-09-915-582-13  
; Sequence 13, Application US/09915582  
; Patent No. US20020120103A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: I7 Human Secreted Proteins  
; FILE REFERENCE: PS723P1  
; CURRENT APPLICATION NUMBER: US/09/915,582  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: PCT/US01/01431  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/231,968  
; PRIOR FILING DATE: 2000-09-12  
; NUMBER OF SEQ ID NOS: 97  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 1867  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-915-582-13

Query Match 34.4%; Score 619.6; DB 10; Length 1867;  
Best Local Similarity 99.4%; Pred. No. 1.9e-138;  
Matches 622; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1175	TGTTATTTCTTCTCTAAATCTTGTGGTACAATACTTGGCCGAAATCTCTCAGGTACGCC	1234
Db	19	TGTGCCCTCTCTCTAAATCTTGTGGTACAATACTTGGCCGAAATCTCTCAGGTACGCC	78



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Db 1106 TTTTCGATTGGATTGGTGTGGAACACCATGCTATCTTACCGTTTCTACGGCAGCCATAC 1165  
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QY 1195 TTGTTGGTACAAATACTTGGCGGAAATCTGCAGTTCAGGCCAACTTTCTTGTGCTGTCA 1254  
Db 1226 TATTGGGAACGTAGTTGGTGTGAGAAATTTGGAGTGGTCTCCCAACAATCCCTGTCGTGTTA 1285  
QY 1255 ATGCTGTGCCTCTCTATACCGGAGAAAAAATGGTTTCATGGAGCCTGGGTTTATTGTTT 1314  
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QY 1375 CTTTCTGGGCAATAGATCTATTTATGCTATGCTATGCTGCTGCTGCTGCTGCTATCC 1434  
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QY 1615 TTTTACTTTGGATATATGGGGTATTTAGACACAGCTTTGGGATAATGCTGGAGCGATTG 1674  
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RESULT 4

US-09-887-576-812  
; Sequence 812, Application US/09887576  
; Patent No. US20020144047A1  
; GENERAL INFORMATION:  
; APPLICANT: Budworth, P.  
; APPLICANT: Brown, D.  
; APPLICANT: Chang, H.  
; APPLICANT: Zhu, T.  
; APPLICANT: Han, B.  
; APPLICANT: Wang, X.  
; APPLICANT: Cooper, Bret  
; TITLE OF INVENTION: Promoters for regulation of plant expression  
; FILE REFERENCE: 1360, 001US1  
; CURRENT APPLICATION NUMBER: US/09/887,576  
; PRIOR FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: US 60/213,848  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/214,087  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/258,692  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 875  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 812  
; LENGTH: 1803  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-09-887-576-812

Query Match 28.1%; Score 506; DB 10; Length 1803;  
Best Local Similarity 58.1%; Pred. No. 2,4e-111;  
Matches 1006; Conservative 3; Mismatches 678; Indels 45; Gaps 5;  
QY 29 GCTGCCCCGGACCCGGGCGAGCAGCAGCAACACAGCTATCAAGATAAAGAGGAAGTTGT 88  
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QY 89 CTTATCGATGAATACTGTTGGGCCCTTACCATAATCTCTCAAGAAACATATAAGTACTTTTC 148  
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QY 149 ACTTCCATTTCTGTGTGGGTCAAAAAAAGTATACGTCTATTACCATGAAACCTCTGGGAGA 208  
Db 210 CTTTCCATTTTGTCAACCACTCTGAGAACCT-- -GCGCATAAATGGGTGGTCTTGGAGA 266  
QY 209 AGCACTTCAAGGGTTGAATTTAGTGGTCTGGGATATTAATTTAAAGATGATGT 268  
Db 267 GGTCTCTGGGTGGAATAGAGCTGATTGATAGTCAGATTGACATAAAGTCTTTAAGAAATGA 326  
QY 269 GATGCCAGCCACTTACTGTGAAATTCATTTAGATAAAGAAAGAGAGATGCAATTTGTATA 328  
Db 327 GGAGAGGGCTCCATTTGTACACTTGAGCTTGATTTCTAAAGAGTTTCACAGTCTTCCGA 386  
QY 329 TGCCATTAATAAATCACTTACTGTTACAGATGTACATAGATGATTTACCAATATGGGTAT 388  
Db 387 TGCCATTTGATACTCATACTGTTTCAGTTTTCATGG-----GTTTTGT 431  
QY 389 TGTGTGTAGGCTGATGAAATGGGAGAGATFACATCTTTTGGACCTATAAANAAGTTGA 448  
Db 432 TGGGAGAGCGGACAAAAACAATGAAACAAGCGTTATCTCTACACACACAAGAGCATCT 491  
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Db 492 TGTCAAAATACAATGATACACAGGATCATGTTAATCTACCCCAAGAGTCTCTTAAGT 551  
QY 509 ACTGGTTCCAAATFACATAAATCCAGATGTCATATTTCAGTAAATGGAAAAAGTCAGATGT 568  
Db 552 TCTTGAAGCTGGTGAAGAAATTTGACATGACATATTCAGTGAAGTGTTCACAACAGATGT 611  
QY 569 GAAATTTGAAGATCGAATTTGACAAATATCTTGATCGGCTCTTTTTCACACATCGGATCA 628  
Db 612 GACCTTTGCACCGCGCTTTGAAAGTATACCTGGATTATCTCTTTTGAGCACACAGATTCA 671  
QY 629 TTGTTTTTCAATTTTCAACTCTTCATGATGTTGATCTTCTTGGTGGGCTTAGTTTCAAT 688  
Db 672 TTGGTTCTCCATTTTCAATCTTTTCATGATGTTATTTTCTCAGTGGTTTGGTTTCAAT 731  
QY 689 GATTTTAAATGAGAACATTAAGAAAGATTATGCTCGGTA---CAGTAAAGAGAGAAAT 745  
Db 732 GATATTGATGCGGACATTCAGAAATGACATATGCAAAAGTATGCTGGAAGATGATGATCT 791  
QY 746 GGATGATATGGATAGAGACCTTAGGAGATGAATATGATGGAACAGGTCATGAGATGT 805  
Db 792 GGAGTCACTGGAGAGAGATGTTAATGAGGAATCTGGATGGAAGCTTGTTCATGGTATGT 851  
QY 806 ATTTAGACCATCAAGTCACCCACTGATATTTCTCTCTCTGATTGGTCTCGGATGTCAGAT 865  
Db 852 ATTTGCCCTCTCGAAGTTTGGCCCTTTCTTCTGAGTTTGGCATCGGCACTCAGCT 911  
QY 866 ATTTGCTGTCTCTCATCTGTTATTTATTTGCAATGATAGAGATTTATATACTG--- 921  
Db 912 GGCAGCTCTTATCTTCTTCTTATTTGTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 971  
QY 922 -----AGAGGGGATCAATGCTCAGTACAGCCATATTTGCTATGCTGCTAGC 968  
Db 972 GCGATATTTGTCAGCGAGGGTCTATCATCACAACCTTTCATTTCTGCTATGCTCTTACA 1031  
QY 969 TCTCCAGTGAATGGTTATTGTCAGAGAACTCTGTATGCTAGACAAG-----AGGAAG 1021  
Db 1032 TCTTTTATTTCTGGCTATGTCAGTGKGGCCCTTACTCAAGGAAATGGTGGTATGGTTAA 1091  
QY 1022 GAGATGGATAAAGCAGATGTTTATTGGGGCATTCCTTATCCAGCTATGTTGTTGGCAC 1081







Db 1511 ACCGATTGTGGGATCCTCATGGCTGGGATCTTGCCCTTCGGCGCCATGTTTCATCGAGC 1570  
QY 1357 TGTATTTTCATCTTCACGCTCTTTCGGGCATATAAGATCTATATGTTCTATGGCTTCATGA 1416  
Db 1571 TCTTCTTCATCTTCAGTGCTATCTGGGAGATCAGTTCTATACCTCTTTGGCTTCCTGT 1630  
QY 1417 TGTGTGTCGTTTATCCTGTGCATTTGACTGTCTGTGACTATTTGTGTGCACATATT 1476  
Db 1631 TCCTTGTGTTTCATCATCCTCGTGTATCTCTGTTTCACAAATCAGCATGTCATGGTGTACT 1690  
QY 1477 TTTCTACTAAATGAGAGATACCGGTGGCAATGGAGCAAGTTTCTCTCTGCTGTCATCAA 1536  
Db 1691 TCCAGCTGTGTCAGAGATATACCGCTGGTGGGAGAAAATTTCTAGTCTCGGGGGCT 1750  
QY 1537 CTGCAATCTATGTTTACATGATTTATCTCTTTACTACTATTTTTCACAAACAAAGATGATG 1596  
Db 1751 CTGCAATCTACGTCCTGGTGTATGCCATCTTTTATTTTCGTTAACAAGCTGGACATCGTGG 1810  
QY 1597 GCTTATTTCAACATCATTTTTACTTTTGGATATATGCGGCTATTAGCACAGCCTTTGGGGA 1656  
Db 1811 AGTTTCATCCCTCTCTCTCTACTTTGGCTACACGGCCCTCATGGTCTTGTCCCTTCGGC 1870  
QY 1657 TAATGTGTGGAGGATTTGGTTTACATGGGAACAAGTGCCTTTTGTCCGAAAAATCTATACTA 1716  
Db 1871 TGCTAACGGGTACCATCGGCTTCTATGCAGCCTACATGTTTGTTCGCAAGATCTATGCTG 1930  
QY 1717 ATGTGAATAATTGACT 1731  
Db 1931 CTGTGAAGATAGACT 1945

RESULT 7  
US-10-201-964-2  
; Sequence 2, Application US/10201964  
; Publication No. US20030008356A1  
; GENERAL INFORMATION:  
; APPLICANT: Ono Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE, A CDNA ENCODING THE SAME, AND USE  
; FILE REFERENCE: OF IT  
; FILE REFERENCE: 062911  
; CURRENT APPLICATION NUMBER: US/10/201,964  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR APPLICATION NUMBER: US/09/762,467  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: JP 10-224308  
; PRIOR FILING DATE: 1998-08-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-201-964-2

Query Match 12.6%; Score 226.4; DB 9; Length 1926;  
Best Local Similarity 52.2%; Pred. No. 1.4e-44;  
Matches 634; Conservative 0; Mismatches 556; Indels 24; Gaps 5;

QY 520 ATACTAAATCCAGATGTCATATTCAGTAAATGGAAAAAGTCAGATGTCGAAATTTGAAG 579  
Db 734 AGAATCAGCTGTACTTCCACTACTCTCTCCACTGGGAGGAAGTGATATCAAAATGGSCCT 793  
QY 580 ATGCAATTTGACAAATATCTTGATCCGTCCTTTTTCACATCGGATTCATGTTTTCAC 639  
Db 794 CTGCTGGGACACTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 847  
QY 640 TTTTCAACTCTCTCATGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 699  
Db 848 TCATTAACCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 907  
QY 700 GACATTTAAGAAAGATTTATGCTCGGTACAGTAAAGAGGAAGAAATGGATGATGGATA 759

Db 908 GGACCCCTCCGGAAGGACATTTGCCAACTACAAAGAGGAGGATGACATTGA----- 956  
QY 760 GAGACCTAGGAGATGAATATGGATGGAAACAGGTGCATGGAGATGATATTTAGACCATCAA 819  
Db 957 -AGACACCATGGAGAGCTGGGTGGAAAGTTGGTGACGGCGAGCTCTTCAGGCCCCCC 1015  
QY 820 GTCACCCACATGAATTTTCTCTCTGATTGGTTCTGGATGTCAGATATATTTGCTGTGTCTC 879  
Db 1016 AGTACCCCATCATCTCCAGCTCCCTGCTGGCTCAGSCATTCAGCTGTTCTGTATGATCC 1075  
QY 880 TCATCGTTATATTTGTCGAATGATGAAGATTTATATACCTGAGA---GGGGATCAATGC 936  
Db 1076 TCATCGTTCATCTTTGTAGCCATGCTTGGGATGCTGCCCTCCAGCGGGAGCTCTCA 1135  
QY 937 TCAGTCAGACCATATTTGTCTATGCTAGCTCCAGTCTCCAGTGAATGTTATTTGGAGGAA 996  
Db 1136 TGACCACAGCCTCGTTCCTCTTCATGTTTCATGGGGGTGTTTGGCGGATTTCTGCTGGCC 1195  
QY 997 GTCTGTATGCTAGACAGGAGGAGATGGATAAAGCAGATCTTTATTTGGGGCATTC 1056  
Db 1196 GTCTGTACCCCACTTTTAAAGGCCATCGGTGGAGAAAGGAGCCTCTGTACGGCACTC 1255  
QY 1057 TTATCCAGCTATGGGTGTGGCACTGCCCTTCTTCATCAATTTTCATAGCCATTTATTAAC 1116  
Db 1256 TGTACCCCTGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 1315  
QY 1117 ATGCTTCAAGAGCATTTCCTTTTGGACAAATGGTGGCGTTTGTGTCATCTGTTTGTG 1176  
Db 1316 ACTCATCAGGAGCGGTGCCCTTTCCCACTAGTGGTGGTCTGTGCTGTCATGTG-GTTCGGG 1374  
QY 1177 TTATTTCTCTCTAAATCTTTTGGTACAATCTTGGCCGAAATCTGTCAGGTCAGGCCA 1236  
Db 1375 ATCTCCCTGCCCTCGTCTACTTGGGCTACTCTTGGCTTCCGAAAGCAG--CCATATG 1432  
QY 1237 ACTTTCCTTGTGTGTCATGCTGTGCTCTATACCGGAGAAATAATGTTTCATGG 1296  
Db 1433 ACAACCTGTGCGCACCAACAGATTTCCCGGCGAGATCCCGAGCAGCGGTGTACATGA 1492  
QY 1297 AGCTCGGGTATTTGTTGCTGGTGGAAATTTACCTTTTGGTTCATCTTTATTTGAAA 1356  
Db 1493 ACCGATTTGGGCAATCCTCATGCTGGGATCTTGGCCCTTCGGGCAATGTTTCATGAGC 1552  
QY 1357 TGTATTTTCATCTTCACGCTCTTCTGGGCATATAAGATCTATATGCTATGGCTTCATGA 1416  
Db 1553 TCTTCTTCATCTTCAGTGTCTATCTGGGAGATCAGTCTCTATACCTCTTTGGCTTCCTGT 1612  
QY 1417 TGTGTGTCGTTATCTCTGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1476  
Db 1613 TCCTTGTGTTTCATCATCTCTGTTGGTATCTCTTTCACAAATCAGCATGTCATGGTGTACT 1672  
QY 1477 TTCTACTAAATGCAGAGATACCGGTGGCAATGGCAAGTTCCTCTCTGCTGCATCAA 1536  
Db 1673 TCCAGCTGTGTGCAGAGGATTTACCGCTGGTGGAGAAATTTCCCTAGTCTCCGGGGGCT 1732  
QY 1537 CTGCAATCTATGTTTACATGATTTCTCTTTTACTACTATTTTTCACAAACAAAGATGATG 1596  
Db 1733 CTGCAATCTACGCTCTGTTTATCCCATCTTTATTTTCGTTAACAACCTGCACATCGTGG 1792  
QY 1597 GCTTATTTCAACATCATTTTACTTTTGGATATATGCGCGTATTTAGCACAGCCTTGGGGA 1656  
Db 1793 AGTTTACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1852  
QY 1657 TAATGTGTGAGCGATTTGTTTACATGGAAACAGTGCCTTTTGGCCGAAAAATCTATACTA 1716  
Db 1853 TGCTAACGGGTACCATCGGCTTCTATGCAGCCTACATGTTTGTTCGCAAGATCTATGCTG 1912  
QY 1717 ATGTGAATAATTGAC 1730  
Db 1913 CTGTGAAGATAGAC 1926

; Sequence 754, Application US/09770791  
; Patent No. US20020062014A1  
; GENERAL INFORMATION:  
; APPLICANT: Gorlach, Jorn  
; APPLICANT: An, Yong-Qiang  
; APPLICANT: Hamilton, Carol M.  
; APPLICANT: Price, Jennifer L.  
; APPLICANT: Raines, Tracy M.  
; APPLICANT: Yu, Yang  
; APPLICANT: Rameaka, Joshua G.  
; APPLICANT: Page, Amy  
; APPLICANT: Matthew, Abraham V.  
; APPLICANT: Ledford, Brooke L.  
; APPLICANT: Woessner, Jeffrey P.  
; APPLICANT: Haas, William David  
; APPLICANT: Garcia, Carlos A.  
; APPLICANT: Krieker, Maja  
; APPLICANT: Slader, Ted  
; APPLICANT: Davis, Keith R.  
; APPLICANT: Allen, Keith  
; APPLICANT: Hoffman, Neil  
; APPLICANT: Hurban, Patrick  
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis  
; FILE REFERENCE: 2029 (PARA-018PRV)  
; CURRENT APPLICATION NUMBER: US/09/770,791  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/178,480  
; PRIOR FILING DATE: 2000-01-27  
; NUMBER OF SEQ ID NOS: 999  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 754  
; LENGTH: 347  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-770-791-754

Query Match 9.6%; Score 172.6; DB 10; Length 347;  
Best Local Similarity 69.3%; Pred. No. 4.7e-32;  
Matches 235; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 1285 AATGGTTCATGAGCGCTGCGGTATGTTGGCTGGGTGGAATTTACCTTTTGGTCAA 1344  
DB 9 AATGGTACTTGACTCCATCAGTCGCTCCCTGATGGGGGTTTGCTACCCCTTTGGAAGCA 68  
QY 1345 TCTTTATTAAGATGATTCATCTTCACTTCACTCTTCTGGGCATATAGATCTATTATGCT 1404  
DB 69 TCTTATGAGATGATCTTGTCTTCCATCTTCCATCTTGGGAATTACAGGCTCTACTATGCT 128  
QY 1405 ATGGCTTCATGATGCTGGTGTGTTATCCTGTGCAATTTGTGACTGTCTGTGACTATTG 1464  
DB 129 ATGGATTCATGTTACTGGTTTGTGATCTCGTCATAGTACGGGTGTCGTGACAATCG 188  
QY 1465 TGTGCACATATTTTCTACTAAATGCAAGATTTACGGGTGGCAATGGACAAGTTTCTCT 1524  
DB 189 TGGGTACATATTTCTGCTGAAATGCAAGAACTATCACTGGCAGTGGACTTCTATTTCT 248  
QY 1525 CTGCTGCATCACTCAACTATGTTTACATGATATTCCTTTTACTACTATTTTCAAAA 1584  
DB 249 CTGCTGCTCGACGGGTGCTATGTTGTTACTTATCTTACTTCTACTACTACTACGTAAGA 308  
QY 1585 CAAAGATGATGGCTTATTTCAACATATTTTACTTTG 1623  
DB 309 CCAAGATGTCGGATTTCTCCAGACAAGCTTCTACTTTG 347

RESULT 9  
US-09-938-842A-798  
; Sequence 798, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SAME, AND METHODS OF USE  
; FILE REFERENCE: SRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 798  
; LENGTH: 1980  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-798

Query Match 9.5%; Score 171.8; DB 9; Length 1980;  
Best Local Similarity 49.2%; Pred. No. 1.5e-31;  
Matches 551; Conservative 0; Mismatches 552; Indels 18; Gaps 3;  
QY 614 TCAACATCGGATTCATTTGGTTTTCAATTTTCAACTCCTTCATGATGGTGTCTCTTGTGT 673  
DB 873 TGATGATCAGATTCATTTGGTTCTCAATCGTTAATCTATGATGATTTGTTCTTCTCTC 932  
QY 674 GGGCTTAGTTTCAATGATTTTAAATGAGACATTAAGAAAAGATTAATGTCGGTACAGTAA 733  
DB 933 TGGTATGGTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992  
QY 734 AGAGGAAGAAATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793  
DB 993 -----GTTAGAGAGTCATGAAGAGGCCCTTCGAGAGACGGGTTGGAATTTGGT 1040  
QY 794 GCATGGAGATGATTTAGACCATCAAGTCACCCACTGATATTTCTCTCTCTGATTTGGTTC 853  
DB 1041 ACACGGAGATGTTTTCAGACCCGCAACAAACCGGAGTTGCTTTGTTGTTATGACAGGAC 1100  
QY 854 TGGATGTCAGATTAATTTGCTGCTCTCATCGTTATTAATTTGTTGCAATGATAGAGATTT 913  
DB 1101 TGGAGTTCAATGCTTTGGAATGATTTTGTCCACCATGATCTTTGCTTGTGCTTGGCTTT 1160  
QY 914 ATATCTGAGAGGGGATCAATGCTCAGTACAGCCATA---TTTGCTATGCTGCTACGTC 970  
DB 1161 ATCTCTCTCAACCGTGGTGGTCTTATGACGGCTATGCTTTTGTCTTGGTGTTCATGGG 1220  
QY 971 TCCAGTGAATGGTTATTTTGGAGGAGTCTGTATGCTAGACAAGGAGGAGGATGATGAT 1030  
DB 1221 ACTATTTGGCAGGATACGCGCTCTTCACGCCCTCTACAAGACGTTTAAGAGGAACCGAATG 1280  
QY 1031 AAAGCAGATGTTTATTTGGGGCATTTCTTATCCAGCTATGCTGTTGGCAGCTGCTTCTT 1090  
DB 1281 AAGAACGCTCTGAAGAACCGCATTCATGTTTCCCGCTACCGCTCTTGTGCTGCTTCTTCT 1340  
QY 1091 CATCAATTTATAGCATTTTATTTACCATCTTCAGAGCATTCTCTTTTGGAAACATGTT 1150  
DB 1341 CCTTAATCGGATTAATCTGGGGACAAAATATCCCGTGCAGTCCCATTTGGTACAAATGTT 1400  
QY 1151 GGGCGTTTGTTCATCTGTTTTTTTTTTTGTATTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1210  
DB 1401 TGCTTTGGTTGCTCTGTTTGGTATCTCTGTTCCACTTGTTCATCGGTGGGTACAT 1460  
QY 1211 TGGCGGAATCTGTCAGGTACGCCCACTTCTTGTCTGTCATGCTGTCCTGCTGCTGCT 1270  
DB 1461 TGGTTTCAGAAAACCTGCACCGGAAGA---TCCAGTGAAGAACCAACAGATCCCGCGCA 1517  
QY 1271 TATACGGAGAAAATGTTTCTCATGAGCTCGGTTATTTGTTGCTGGGTGGAAATTT 1330  
DB 1518 GATCCCAACACAGGCTTGGTATCATGAACCAATCTTCTCCATTTTGGTGGAGGATCT 1577  
QY 1331 ACCTTTTGGTTCAATCTTTTATTGAAATGATTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 1390

Db 1578 CCCATTTGGCGCAGTCTTCATCGAGCTCTTCTTCATACCTACCCCAATATGGCTACATCA 1637  
Qy 1391 GATCTATTATCTCTATGCTCATGCTGGTGTCTGCTGTTATCTGCTGCAATTTGGACTGT 1450  
Db 1638 GTTCTACTACATATCGGCTCCCTCTCACTGCTCTTCACTATTTTGATCATCACTTGGCG 1697  
Qy 1451 CTGTGTGACTATTGTGTCACATATTTTCTACTAAATGCGAAGATTACCGGTGGCAATG 1510  
Db 1698 AGAGATCACGGTCTGCTCTCTTATTTTTCAGCTGTGTAGTGAAGACTATCAATGGTGTG 1757  
Qy 1511 GACAAAGTTTCTCTGCTGCTCACTCACTGCAATCTATGTTTACATGATATCTCTTTACTA 1570  
Db 1758 GAGATCTTACTTAACTACATCAGGCTCTTCGGGGTTTACTCTCTTCTTACGCACTCTTTA 1817  
Qy 1571 CTATTTTTCACAAACAAAGTATGCTGTATTTTCAACATCATTTTACTTTTGGATATAT 1630  
Db 1818 CTTCTACACCAAACTTGAGATCAACAAAGCTCGTCTCTGCACTGCTCTACTTTGGGTACAT 1877  
Qy 1631 GCGCGTATTAGCACAGCCTTGGGATAATGTGTGGAGCGATTGGTTACATGGGAACAAG 1690  
Db 1878 GCTCATAGTTTCATACGATTTCTTCGCTCTTACTGGTGCAATGGTTTCTACGCATGCTT 1937  
Qy 1691 TGCCTTTTTCGGAATAATCTATACTAATGTGAAATTTGACT 1731  
Db 1938 TTGGTTTACCAGGCTTATCTACTCTTCGGTTAAATCGAAT 1978

RESULT 10  
US-09-910-664-30/c  
; Sequence 30, Application US/09910664  
; Publication No. US2002019464A1  
; GENERAL INFORMATION:  
; APPLICANT: POGUE, Greg P.  
; APPLICANT: DELLA-CIOPPA, Guy R.  
; APPLICANT: WOLFE, Gerson M.  
; APPLICANT: ZHENG, Wenjin  
; TITLE OF INVENTION: METHODS OF CREATING DWARF PHENOTYPES IN  
; FILE REFERENCE: 00801018900US01  
; CURRENT APPLICATION NUMBER: US/09/910,664  
; CURRENT FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 1132  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-910-664-30

Query Match 9.4%; Score 170; DB 9; Length 1132;  
Best Local Similarity 50.0%; Pred. No. 3.3e-31;  
Matches 481; Conservative 0; Mismatches 475; Indels 6; Gaps 2;

Qy 782 ATGGAACAGGTGCATGAGATGATTTTATAGACCATCAAGTCACCCACTGATATTTTCCCTC 841  
Db 1132 ATGGAAGCTGTACACGAGATGCTTCAGGCCACCGGTGAACCTCTGTTTATTTGTGTGT 1073  
Qy 842 TCTGATTTGTTCTGATGTCAGATATTTGCTGTGCTCTCTCATGTTATTTATTTGCAAT 901  
Db 1072 TTAGTTTGTACAGGTGTTTCAGATCTTCGGAATGTCACCTTGTACAAATGATTTTGGGTT 1013  
\*Qy 902 GATAGAGATTTTATATCTCAGAGGGGATCAATGCTCAGTACAGCCATAATTGTC---TA 958  
Db 1012 GCTTGGCTTCTTATCTCCATCCACAGAGAGGCGCTTATGACGTGCCATGTTCTTCTGTG 953  
-Qy 959 TGCTGTACTCTCCAGTGAATGGTTATTTTGGAGGAAGTCTGTATGCTAGACAAAGGAGG 1018  
Db 952 GGTTTTTCATGGGCATATTCCTGTTACTCTCTCGCTTCACAAAATGTTCAAAGG 893  
Qy 1019 AAGGAGATGATTAAGCAGATGTTTATTTGGGGCATTTCCCTTATCCAGCTATGGTGTGG 1078  
Db 892 AAACAAGTGAAGAGATGACCTTGAAGACTGCATTCATGTTTCCCGGTATCCTTTTTCG 833

Qy 1079 CACTGCCCTTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAGCCATTCCTTT 1138  
Db 832 TATCTTCTTTTCTTGAATGCCCTTATTTGGGAGACAGATCATCTCGGAGCCATACCAT 773  
Qy 1139 TGSAAACAATGGTGGCCGTTTGTTCATCTCTGTTTGTATTTTCTCTCTCTCTCTCTCTCT 1198  
Db 772 TGTACAAATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 713  
Qy 1199 TGGTACAAATGTTGGCCGAATCTGTCTAGGTCAGCCCACTTTCTCTCTCTCTCTCTCTCT 1258  
Db 712 TGGTAGATCTATCTGGGTTTACAAAGCCAG---CAATTTGAAGATCCAGTCAAAACAAACA 656  
Qy 1259 TGTGCCCTCGTCTTACCGGAGAAAAATGTTTCTCAGAGCTCGGCTTATTTGTTGCC 1318  
Db 655 GATCCCGAGGCAAGTACCAGAGAGCCGTTGGTACATGAAACCACTTTTCTCTATACATA 596  
Qy 1319 GGTGGGAATTTTACCTTTTGGTTCATCTCTTATTTGAATGATTTTCACTCTTCAGCTCT 1378  
Db 595 TGGAGGCAATTTCTCCCGTTTGGAGCAGTCTTCACTCGAGCTCTTCTCATCTTGACATCTAT 536  
Qy 1379 CTGGGCATATAAGATCTATTTATGCTATGCTTCACTCATGATGCTGGTCTGTTTATCTCT 1438  
Db 535 ATGGCTGAACCAAGTCTTACTACATCTTCCGGTTCCTCTTTATAGTCTTTTGTGATCTT 476  
Qy 1439 CATTTGACTCTCTCTGCTGACTATTTGTGTCACATATTTTCTACTAAATGCAGAAATTA 1498  
Db 475 CGTCACCTGTGCAGAGATCACAGTGGTCTCTGCTACTTCCAGCTTTGTAGCGAGACTA 416  
Qy 1499 CCGGTGCAATGGACAAAGTTTCTCTCTGCTGCATCACTCAATCTATGTTTACATGTA 1558  
Db 415 CAACTGGTGTGGAGAGCTTACTTAACTGCGGCTCATCCGCTTCTACCTTCTTCCCTCTA 356  
Qy 1559 TTCCTTTTACTACTATTTTTCAAAACAAGATGATGGCTTATTTTCAAAACATCATTTTA 1618  
Db 355 CTCAATCTTCTACTTCTTCAAAAGCTGGAGATCACAAAGCTAGTCTCGGGAATGCTCTA 296  
Qy 1619 CTTTGGATATATGCGGTATTTAGCACAGCTTGGGATAATGTTGGAGCGATTGGTTA 1678  
Db 295 CTTGCGGTACATGATTAATCATCTCTTACGATTTCTCGTCTTAACCTGGCAATCGGTTT 236  
Qy 1679 CATGGGAACAAGTGCCTTTGTCGAAAAATCTATACATAATGTGAAAAATGACTAGAGAC 1738  
Db 235 CTATGCTTGTCTCTGTTCTGTGAGAAAGATCTACTCTCAGTGAAGATTGACTAGAACCC 176  
Qy 1739 CA 1740  
Db 175 AA 174

RESULT 11  
US-09-887-576-471  
; Sequence 471, Application US/09887576  
; Patent No. US20020144047A1  
; GENERAL INFORMATION:  
; APPLICANT: Budworth, P.  
; APPLICANT: Brown, D.  
; APPLICANT: Chang, H.  
; APPLICANT: Zhu, T.  
; APPLICANT: Han, B.  
; APPLICANT: Wang, X.  
; APPLICANT: Cooper, Bret  
; TITLE OF INVENTION: Promoters for regulation of plant expression  
; FILE REFERENCE: 1360.001US1  
; CURRENT APPLICATION NUMBER: US/09/887,576  
; CURRENT FILING DATE: 2001-06-25  
; PRIOR APPLICATION NUMBER: US 60/213,848  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/214,087  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/258,692  
; PRIOR FILING DATE: 2000-12-29  
; NUMBER OF SEQ ID NOS: 875



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: APPLICANT: Secrist, Heather
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
:
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
:
: FILE REFERENCE: 210121.527
:
: CURRENT APPLICATION NUMBER: US/09/878,178
:
: CURRENT FILING DATE: 2001-06-08
:
: NUMBER OF SEQ ID NOS: 2237
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 1582
:
: LENGTH: 350
:
: TYPE: DNA
:
: ORGANISM: Homo sapien
:
: US-09-878-178-1582

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	Query Match	5.6%;	Score 100.8;	DB 9;	Length 350;
	Best local Similarity	57.2%;	Pred. No. 6.5e-15;		
Matches 183;	Conservative 0;	Mismatches 137;	Indels 0;	Gaps 0;	
Qy	1242	CCTTGTCGTGTCGAATCGTGCCTCCTATACGGAGAAATAATGTTCCATGGAGCCT	1301		
Db					
Db	28	CCAGTTCGAACAATCACATTCCAGCTCAGATCTCTGAACAGTCGTTCTCACGAAGAACC	87		
Qy	1302	CGCGFTATTGTTGCCCTGGTGGGAATTTTACCTTTTTGGTTCCAACTTTATTGAAAATGTAT	1361		
Db					
Db	88	TGCTCGTATTATCATGGGAGGGATTTTGCCCTTTGGCTGCATCTTTATACAACCTTTC	147		
Qy	1362	TTCACTTTCACGCTCTTCTGGGCATATAAAGATCTATTATGTCTATGGCTTCATGANTGTG	1421		
Db					
Db	148	TTCACTTCGAATAGTATTTTGGTTCACACAGATGATTACATGTTTGGCTCTATTCTTG	207		
Qy	1422	GTGCTGGTTATCCGTGCATTGTGACTGCTCTGTGACTATTGTGTCACATATTTTCTA	1481		
Db					
Db	208	GTGTTTATCATTTTGGTTTATTACCTGTCTGAAAGCAACTATACCTTCTTGCTATTCTCCAC	267		
Qy	1482	CTAAATGCAGAAAGATTACCGGTGGCAATGGACAAGTTTCTCTCTGCTGCATCAACTGCA	1541		
Db					
Db	268	CTATGTGCAGAGGATTATCATTTGGCAATGGCTTCATTCTTACGATGGCTTTACTGCA	327		
Qy	1542	ATCTATGTTTACATGTATPCT	1561		
Db					
Db	328	GTTTATTTCTTAATCTATGC	347		

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RESULT 15
US-09-910-943-687
; Sequence 687, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/1G1448U$1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 687
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(744)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-687

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	Query Match	5.5%	Score 99.4	DB 10	Length 744
	Best Local Similarity	52.6%	Pred. No. 1.9e-14		
	Matches 271	Conservative	0	Mismatches 228	Indels 16
	Gaps	2			
QY	592	AAATCTTGATCGTCGCTCTTTTCAACATCGGATCATTTGGTTTTCAAATTTCAACTCCT	651		
Db	100	ATATNTTTTATGAATCATCGCTCACACACATCATGTTTATGATTTATGATTCGT	159		

Qy	652	TCATGATGGTGATCTCTCTGGTGGGCTTAGTTTCAATGATTTTAATGAGAAACATTAAGAA	711
Db	160	TGGTGATTTGGCTCTCCCTTTCGGGTATGGTGTCTATGCTTAAGGACATTAACATA	219
Qy	712	AAGATTATGCTCGGTACAGTAAAGAGGAAGAAATGGATCATATGATAGAGACCTAGGAG	771
Db	220	AGATATTGCAAGGTACATCATGATGGATTCTACGGAAGATGCTCA-----AG	267
Qy	772	ATGAATATGGATGGAACAGAGGTGCATGGAGATCTATTATAGACCATCAAGTCACCCACTGA	831
Db	268	AAGAAATTTGGGTGGAAGCTGGTTCATGGTGATATTTTCAGAGCACCAGAAAGGATGC	327
Qy	832	TATTTCCCTCTCGATTGGTCTGGGATGTCAGATATTTGCTGTGCTCTCATCGTTATTA	891
Db	328	TGCTCTCTGTTTTCCCTGGGTTCTGGGGCTCAGATCTCAATATGACTTTTGTGCACATTA	387
Qy	892	TTGTTGCAATGATAGAGAATTTATATACTCAGAGGGGATCAATGCTCAGTACAGCCATAT	951
Db	388	TTTTTGGCTGCCCTTGGATTTTTTGTCCCTGCTAACAGAGGTGCTCTCAATGACATGTGCTG	447
Qy	952	TTGCTCATGCTGCTACGTCT----CCAGTGAAATGGTATTTTGGAGGAAGTCTGTATGCT	1007
Db	448	TCCGTGCTGTGGGTGTGGTGTGGAACCTCAGCTGGTATGTGTGCTCAAGATTTTACAAA	507
Qy	1008	AGACAAGGAGGAGAGATGGATAAAGCAGATGTTTATTTGGGGACCTCCTTATCCCAGCT	1067
Db	508	TCATTTCGTSGAGAAAGTCGAACGAATGCTTACTGACTGCATCTCTCTGCCCCAGGG	567
Qy	1068	ATGGTGTGTGGCACTGCCCTCTTTCATCAATTTCAAT	1102
Db	568	ATTGNAATTCGCTGATTTCTCTCTTAATGAACCTTAAT	602

Search completed: January 20, 2003, 15:45:17  
Job time : 152 secs







US-08-959-004-6

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*Query Match          12.6%; Score 227.6; DB 4; Length 2805;
Best Local Similarity 51.9%; Pred. No. 1.5e-50;
Matches 596; Conservative 0; Mismatches 534; Indels 18; Gaps 3;

QY: 592 AATATCTTGATCGCTCTCTTTTCAACATCGGATTCATTGGTGTTCCTCAATTTTCAACTCTCT 651
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1044 ACTATATCTGGAGTCTATGCCTCATACCCACATTCAGTGGTTAGCATTAATCAATTCCTC 1103

QY 652 TCATGATGGTGATCTCTTGGTGGGCTTAGTTTCAATGATTTTAAATGAGAAATTAAGAA 711
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1104 TGGTCATTTGTTCTTCTTATCTGAATGGTAGCTATATGTTTACGGACACTGCACA 1163

QY 712 AAGATTATGCTCGGTACAGTAAGAGGAAGAATGGATCATATGGATAGAGACCTAGGAG 771
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1164 AAGATATGCTAGATATAATCAGATGGACTCTACGGAAGATGCCAG-----G 1211

QY 772 ATGAATATGGATGGAAACAGTGCATGGAGATGTTATTAGACATCAAGTCACCCACTGA 831
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1212 AAGAAATTTGGCTGGAACCTGTTTCATGGTGATATTCGCTCTCAAGAAAGGATGC 1271

QY 832 TATTTTCCCTCTGATGGTCTCGGATGTCAGATATTTGCTGTGCTCTCTCATCGTTATTA 891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1272 TGCATATCACTCTTTAGGATCCGGACACAGATTTTAATATGACCTTTGTGACTCTAT 1331

QY 892 TTGTTGCAATGATAGAGATTTATATACAGAGAGGGATCAATGCTCAGTAC---AGCCA 948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1332 TTTTGGCTTGGCTGGGATTTTGTACCTTGCCACCGAGGAGCGGTGATGAGCGTGTGCG 1391

QY 949 TATTTTGTCTATGCTGTAGTCTCCAGTGAATGGTATTTTGGAGGAATCTGTATGCTA 1008
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1392 TGGTCTGTGGTGTGCTGGGACCCCTGCAGGCTATGTTGCTGCCAGATCTATAAGT 1451

QY 1009 GACAGGAGGAGAGAGATGGATAAGACAGATGTTATTGGGGCATTCCTPTATCCAGCTA 1068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1452 CCTTTGGAGGTGAGAAGTGGAACAAATGTTTTATTAACATCATTTCTTTGCTCGTGGGA 1511

QY 1069 TGGTGTGGCCACTGCCCTTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAG 1128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1512 TTGATTTTCTGCTGACTTCTTTATTAATGAATCTGATCCTCTGGGGAAGGATCTTCAGCAG 1571

QY 1129 CCATTTCTTTTGGAAACAATGTGGCGGCTTTGTTGGCATCTGTTTTTTTGTATTCTTCCTC 1188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1572 CTATTTCTTTTGGACACGTTTGGCATATATGSCCTTTTGGTTCTGCATATCTGTGCTC 1631

QY 1189 TAAATCTTGTGTACATACTTGGCCGAAATCTGTACAGTCAAGCCCACTTTCCTTGTCTC 1248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1632 TGACGTTTATTTGGTGCACTACTTTTGGTTTTTAAAGAAGAAATGCCATTTGAACAC---CCAGTTTC 1688

QY 1249 GTGTCAATGCTGTGCTCGTCTATACGGGAGAAAATGGTTTCATGGAGCCTGCGGTTA 1308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1689 GAACCAATCAGATTTCCAGTCAAGATTCCTGACAGTCGTTCTACAGAAAGCCCTTGCCCTG 1748

QY 1309 TTGCTTGGCTGGGTGGAATTTTACCTTTTGGTTTCAATCTTTATTGAAATGATTTTCACTC 1368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1749 GTATTATCATGGAGGATTTTGGCCTTTGGCTGTCATCTTTATACAACTTTTCTTCATTC 1808

QY 1369 TCAGTCTTTTCGGGCATATAAAGATCTATTATGCTATAGGCTTCATGATGCTGGTGTGCTGG 1428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1809 TGAATAGTATTTTGGTCACACCAAGATGATTTACATGTTTGGCTTCTCTATTTCTTGGTGT 1868

QY 1429 TTATCTGTGCAATTCGACTGTCTGTGTGACATTTGTGTGCACATATTTTCTACTAAATG 1488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1869 TCATTTTGGTTATTTACCTGTCTTGAAGCAACTATATCTCTTTTGGTATTTTCCACCTATGTG 1928

QY 1489 CAGAAGATTACCGGTGGCAATGGCAAGTTTCTCTCTGCTGCATCAACTCAACTCAATCTATG 1548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1929 CAGAGATTATCATTTGGCAATGGCTTCACTCTTACAGAGTGGCTTTACTGCAGTTTATT 1988

QY 1549 TTTTACATGATTTCTTTTACTACTATTTTTCATAAACAAGATGATGCTTATTTTCAAA 1608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1989 TCTTAATCTATGCATACACTACTTCTTTTCAAAACTGCAGATCATCGGGAACAGCAAGCA 2048
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QY 1609 CATCATTTTACTTTTGGATATATGCGGTATTTAGCACAGCCTTTGGGATAAATGTGTGGAG 1668
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2049 CAATTCTGTACTTTGGTTATACCATGATTAATGGTTTGTGATCTTCTTTTACAGGAA 2108

QY 1669 CGATTGGTTTACATGGGAACAAGTGGCTTTTGCCGAAAAATCTATACATAATGTGAAAAATTG 1728
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2109 CAATTGGCTTCTTTGCAATGCTTTTGGTTTGTGTACCAAAATATACAGTGTGGTGAAGGTTG 2168

QY 1729 ACTAGAGA 1736
    ||| ||| |||
Db 2169 ACTGAAGA 2176
    ||| ||| |||
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RESULT 2

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US-09-385-982-530/c
; Sequence 530, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: 11
; FILE REFERENCE: CCDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(769)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-530
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Query Match 5.1%; Score 91.6; DB 4; Length 769;

Best Local Similarity 57.0%; Pred. No. 7.1e-15;

Matches 166; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

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QY 1261 TGCCTCGTCTATACCGGAGAAAAATGTTTCATCGAGCCTGCGGTATTGTTTGCCTGG 1320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 308 TCCACNGTCAGATTCCTGAACAGTCGTTCTACACGAAGCCCTTGCCTGATTAATCATGG 249

QY 1321 GTGGAATTTTACCTTTTGGTTCAATCTTTATTGAATGATTTTCATCTTCAGCTCTTTCT 1380
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 GAGGATTTTGGCCTTTTGGCTGCATCTTTATACAACTTTTCTTCATCTGAAATGATATT 189

QY 1381 GGGCATATAAGATCTATTATGCTTATGGCTTCATGCTGCTGCTGTTATCTCCTGCA 1440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 GGTACACACAGATGATTACATGTTTGGCTTCCTATTCTGCTGTTTATCATTTTGGTTA 129

QY 1441 TTGTGACTGTCTGTGACTATTGTTGTGCACATATTTTCTACTAAATGCAGAAATACC 1500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 TTACCTGTTCTGAAGCAACTATATCTTTGCTATTTTCCACCTATGTGCAGAGGATTATC 69

QY 1501 GGTGGCAATGGACAAGTTTCTCTCTGCTGCATCAACTGCAATCTATGTTT 1551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 68 ATTGGCAATGGCTTCATTCTCTTACAGTGGCTTTACTGCCAGTTTATTCTT 18
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RESULT 3

US-08-232-463-14

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

APPLICANT: DORNER, F.  
 APPLICANT: SCHEIFLINGER, F.  
 APPLICANT: FALKNER, F. G.  
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 NUMBER OF SEQUENCES: 52  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: 1800 Diagonal Road, Suite 500  
 CITY: Alexandria  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22313-0299  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/232,463  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/07/935,313.  
 FILING DATE:  
 APPLICATION NUMBER: EP 91 114 300.6  
 FILING DATE: 26-AUG-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BENT, Stephen A.  
 REGISTRATION NUMBER: 29,768  
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)836-9300  
 TELEFAX: (703)683-4109  
 TELEX: 899149  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7218 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: ptz9pt-F1s  
 PS-08-232-463-14

[illegible]

Db	1464	TTG	1466
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1  RESULT 4
2  US-08-232-463-14/c
3  ; Sequence 14, Application US/08232463
4  ; Patent No. 5670367
5  ; GENERAL INFORMATION:
6  ; APPLICANT: DORNER, F.
7  ; APPLICANT: SCHEIFELINGER, F.
8  ; APPLICANT: FALKNER, F. G.
9  ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
10 ; NUMBER OF SEQUENCES: 52
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Foley & Lardner
13 ; STREET: 1800 Diagonal Road, Suite 500
14 ; CITY: Alexandria
15 ; STATE: VA
16 ; COUNTRY: USA
17 ; ZIP: 22313-0299
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/232,463
25 ; FILING DATE:
26 ; CLASSIFICATION: 435
27 ; PRIOR APPLICATION DATA:
28 ; APPLICATION NUMBER: US/07/935,313
29 ; FILING DATE:
30 ; APPLICATION NUMBER: EP 91 114 300.6
31 ; FILING DATE: 26-AUG-1991
32 ; ATTORNEY/AGENT INFORMATION:
33 ; NAME: BENT, Stephen A.
34 ; REGISTRATION NUMBER: 29,768
35 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: (703)836-9300
38 ; TELEFAX: (703)683-4109
39 ; TELEFAX: 899149
40 ; INFORMATION FOR SEQ ID NO: 14:
41 ; SEQUENCE CHARACTERISTICS:
42 ; LENGTH: 7218 base pairs
43 ; TYPE: nucleic acid
44 ; STRANDEDNESS: single
45 ; TOPOLOGY: linear
46 ; IMMEDIATE SOURCE:
47 ; CLONE: pt2qpt-Fls
48 ; US-08-232-463-14

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[illegible]



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; FEATURE; unsure
; NAME/KEY: unsure
; LOCATION: (157)
; FEATURE;
; NAME/KEY: unsure
; LOCATION: (161)
; FEATURE;
; NAME/KEY: unsure
; LOCATION: (204)
; FEATURE;
; NAME/KEY: unsure
; LOCATION: (239)
; FEATURE;
; NAME/KEY: unsure
; LOCATION: (305)
US-09-175-928-20

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Query Match 2.5%; Score 45.6; DB 4; Length 519;  
Best Local Similarity 47.5%; Pred. NO. 0.0085;  
Matches 160; Conservative 0; Mismatches 174; Indels

Qy	769	GAGATGAATATGGATGGAACAGGTGCATPGAGATGTATTATAGACCATCAAGTCACCCAC	828
Db	149	GGAAAGAANTGNCTGGAAACTTGTTCATGTGTATATACCGTCTCCAGAANAAGGGA	208
Qy	829	TGATATTTTCCCTCTCGATTGGTCTTGAGATGCAGATATTGCTGTCTCATCGTTA	888
Db	209	TGCTGCTATCAGTCTTTCTTAGGAGCCGGANACAGATTAATAATGACCTTTGTGACTC	268
Qy	889	TTATTGTTGCAATGATAGAAGATTTTATACTAGAGGGGATCAATGCTCAGTACA---	945
Db	269	TATTTTTCGCTTGCCCTGGGAGTTTTGTCACTCCCANCCGAGGAGCCGTGATGACGTGTG	328
Qy	946	CCATATTTTGTTCTATGCTGTACGTCTCCAGTGAATGGTTATTTTGGAGGAAGTCTGTATG	1005
Db	329	CTGTGTCCTGTGGGTGCTGCTGGCACCCCTGCAAGGCTATGTTTCTGCCAGATCTTATA	388
Qy	1006	CTAGACAAGGAGGAGGAGATGGATTAAGCAGATGTTTATTTGGGGCATTCCTTTATCCAG	1065
Db	389	AGTCCTTTGGAGGTGAGAAGTGGAAAACAAATGTTTTATTAACATCATTCCTTTGTCTGT	448
Qy	1066	CTATGTGTGTGGCACTGCCTTCTTCATCAATTTTCAT	1102
Db	449	GGATTCGTATTGCTGACTCTCTCTTATTAATGAATCTCAT	485

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RESULT 7
US-09-798-096-10/c
; Sequence 10, Application US/09798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQ12 EXPRESSION
; FILE REFERENCE: PFS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

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	Query Match	2.5%	Score 44.6;	DB 4;	Length 99500;
	Best Local Similarity	46.3%	Prsd. No. 0.15;		
	Matches 146;	Conservative	0;	Mismatches 169;	Indels 0; Gaps 0;
QY	507	AAACTGGTTC	CAAAATCA	AAAAATCCAGATGTCATATTCAGTAAATG	GGAAAAAGTCAGAT 566
DB	9936	ATACAGTTTT	CAAAATAGCT	ACGAAGGAGGATATTTGAATGCTCCCAACACACA	CAAGAAATGATAA 9877

	Qy	567	GTGAATTTGACAGTCGATTGGACAATAATCTTGTAATCCGTCCTTTTTTCAACATCGGATT	626
	Db	9876	ATGTTTTAAGATGATAGATATGCTAAATTACCCTGCATCATCAITATACAGTATATGTTAT	9817
	Qy	627	CATTGGTTTTCAATTTTCAACTCCTTCATGATGGTGATCTTCTTTGGTGGGCTTAGTTTCA	686
	Db	9816	CAAATATCACATATGTACCCCATAAATTTGGGGGTACAATATGTCACTTTAAAGAAT	9757
	Qy	687	ATGATTTTACAGAACATTAAAGAAAAGATTATGTCGCTACAGTAAGAGAGGAAGAAATG	746
	Db	9756	GTA AAAATAAAAAAGTCATTGCAC TAAAATTATGTTAAATCCACTTAAAAAGCCAAGTA	9697
	Qy	747	GATGATATGGATAGAGACCTAGGAGATGAATATGATGGAAACAGGTGCATGGAGATGTA	806
	Db	9696	GAAGATATCTGCTACACCTATGTAAATGTGTATGTACGTATATATATAAAAAATGTAGATAAC	9637
	Qy	807	TTTAGACCATCAAGT	821
	Db	9636	TATATATAAATATGT	9622
		RESULT 8		
		US-08-909-965C-9		
	:	: Sequence 9, Application US/08909965C		
	:	: Patent No. 5936078		
	:	: GENERAL INFORMATION:		
	:	: APPLICANT: Kuga Tetaro		
	:	: APPLICANT: Nakagawa Satoshi		
	:	: APPLICANT: Sakaki yoshiyuki		
	:	: APPLICANT: Zhao Nanding		
	:	: APPLICANT: Hashida Hideji		
	:	: TITLE OF INVENTION: NOVEL DNA, NOVEL POLYPEPTIDE		
	:	: TITLE OF INVENTION: AND NOVEL ANTIBODY		
	:	: NUMBER OF SEQUENCES: 17		
	:	: CORRESPONDENCE ADDRESS:		
	:	: ADDRESSEE: FITZPATRICK, CELLA, HARPER AND SCINTO		
	:	: STREET: 277 Park Avenue		
	:	: CITY: New York		
	:	: STATE: New York		
	:	: COUNTRY: U.S.A.		
	:	: ZIP: 10172-0194		
	:	: COMPUTER READABLE FORM:		
	:	: MEDIUM TYPE: Floppy disk		
	:	: COMPUTER: IBM PC compatible		
	:	: OPERATING SYSTEM: PC-DOS/MS-DOS		
	:	: SOFTWARE: PatentIn Release #1.0, Version #1.25		
	:	: CURRENT APPLICATION DATA:		
	:	: APPLICATION NUMBER: US/08/909,965C		
	:	: FILING DATE: August 12, 1997		
	:	: CLASSIFICATION: 514		
	:	: PRIOR APPLICATION DATA:		
	:	: APPLICATION NUMBER: JP 322745/95		
	:	: APPLICATION NUMBER: PCT/JP96/03630		
	:	: FILING DATE: 12-No. 5936078-1995		
	:	: FILING DATE: 12-Dec-1996		
	:	: ATTORNEY/AGENT INFORMATION:		
	:	: NAME: Lawrence S. Perry		
	:	: REGISTRATION NUMBER: 31865		
	:	: TELECOMMUNICATION INFORMATION:		
	:	: TELEPHONE: 212-758-2400		
	:	: TELEFAX: 212-758-2982		
	:	: TELEX: 236262		
	:	: INFORMATION FOR SEQ ID NO.: 9:		
	:	: SEQUENCE CHARACTERISTICS:		
	:	: LENGTH: 882 base pairs		
	:	: TYPE: nucleic acid		
	:	: STRANDEDNESS: double		
	:	: TOPOLOGY: linear		
	:	: MOLECULE TYPE: cdna to mRNA		
	:	: ORIGINAL SOURCE:		
	:	: ORGANISM: human		
	:	: IMMEDIATE SOURCE:		
	:	: CLONE: Fl180		

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; FEATURE:
; - NAME/KEY: CDS
; - LOCATION: 97 to 195
; - IDENTIFICATION METHOD: by experiment
;
us-08-909-965C-9
Query Match
  2.3%; Score 42.2; DB 2; Length 882;
Best Local Similarity 51.9%; Pred. No. 0.085;
Matches 95; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1554 ATGTATTCCTTTTACTACTATTTTTCACAAACAAGATGATGGCTTATTTTCAACACATCA 1613
Db 19 ATCTATGTCAGTACACTACTCTCTTTTCAAACTGTCAGATCACGGCAACAGACACAAT 78

QY 1614 TTTTACTTTGGATATGCGCGTATTAGCACAGCCTTGGGGATAATGTGTGGGCGATT 1673
Db 79 CTGTACTTTGGTTATACCATGATAATGGTTTGTGATCTCTTCTTTTACAGGAACAAT 138

QY 1674 GOTTACATGGGAACAAGTGCCCTTTGTCGAAAAATCTATACTAATGTGAAAAATGACTAG 1733
Db 139 GCCTTCTTGGCATGCTTTTGGTTTGTACCAAAATATACAGTGTGTGAAGGTTGACTGA 198

QY 1734 AGA 1736
Db 199 AGA 201

RESULT 9
US-09-134-001C-931
; Sequence 931, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 931
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-931

Query Match
Best Local Similarity 43.5%; Score 38.8; DB 4; Length 1707;
Matches 175; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

QY 202 TGGGAGAGCCTTCAAGGGTTGAATTTAGTGGCTGGGATATTAATTTAAAG 261
Db 500 TTGGTGAAGAGCTGAACCACTTGAATCGAAATCGAAATTTATGAGCCCAAGTTAAATG 559

QY 262 ATGATGTGATGCCGCCCACTTACTCTGAAATTTAGATAAAGAGAGAGATGCAT 321
Db 560 AATATGAGAAATTTAAAGTGAAGTAATATGTTCAAGCTCATATACATGTCGCT 619

QY 322 TTGTATGCCATAAAATCAATTTACTGTCACAGATGTACATGATGATTTACCAATAT 381
Db 620 TAGAAGATCAAAATTTAAATTTAAATCTTATATGATGATCAATTTCCAGAATTAATTCGAG 679

QY 382 GGGGTATTGTTGGTGAGGCTGTAGAAAATGGGAGAGATTAATCTTTGGACCTATAAAA 441
Db 680 AAACCTCAAAAAGAAATTTACCAGGACAGTTTCAAGATTTTAAAAATATGGATGTAGAGACTTAA 739

QY 442 AACTTGAATAGTTTTTAATGAAATCGAATTTGTGATGTTAACTTAATCTACTAGTGAAGAA 501
Db 740 AGGTTGAAGGCTGATTTTAGACCATGTCAAGTGCATGGGTGATACAAATACAAAGCTCTTAAGA 799
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QY 502 AGGTGAAACTGGTTCCTCAAAATATAAATCCAGATGTCATATTCAGTAATAAATGAAAAAGT 561
Db 800 CAGAATTAAGTTTGTGTAACCAATGATTAGTCGATTAGAATTGAGCTAAGCTAATAATA 859

QY 562 CAGATCTCAAAATTTGAAAGATCGATTTTGACAAATATCTTTGATC 603
Db 860 AACTTTGAAATATTAAATGATAAAATTAGATAAATGATAATGATATGATC 901

RESULT 10
US-09-564-805-28/c
; Sequence 28, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (910)..(13104)
; OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
; OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
; OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
; OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
; NAME/KEY: misc_feature
; LOCATION: (13756)..(22917)
; OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
; OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
; OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
; OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
; NAME/KEY: misc_feature
; LOCATION: (23045)..(26452)
; OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
; OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
; OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
; OTHER INFORMATION: signal: 26447-26452
; NAME/KEY: variation
; LOCATION: (826)..(23879)
; OTHER INFORMATION: s at positions 826 and 23180 is G or C; y at
; OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
; OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
; OTHER INFORMATION: positions 22211 and 23879 is A or G.
US-09-564-805-28

Query Match
Best Local Similarity 48.9%; Score 38.8; DB 4; Length 26664;
Matches 133; Conservative 0; Mismatches 137; Indels 2; Gaps 1;

QY 436 ATAAAAAATCTTGAATAGTGTATTAATGGAATCGAATTTGATGATCTTAATCTAATG 495
Db 11736 AAAGAAAAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 11677

QY 496 AAGGAAAGGTGAAATGCTGCTCAAAATCAAAATCAAAATCAAAATCAAAATCAAAATCA 555
Db 11676 CAGAAATCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 11617
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;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/329,154  
;; FILING DATE: 25-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/161,907  
;; FILING DATE: 02-DEC-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/985,321  
;; FILING DATE: 04-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/429,791  
;; FILING DATE: 31-OCT-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: INGOLIA, DIANE E.  
;; REGISTRATION NUMBER: 40,027  
;; REFERENCE/DOCKET NUMBER: OPHD-01763  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 705-8410  
;; TELEFAX: (415) 397-8338  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8133 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..8130  
US-08-480-604A-5

Query Match 2.1%; Score 37.8; DB 1; Length 8133;  
Best Local Similarity 44.2%; Pred. No. 3.2;  
Matches 156; Conservative 0; Mismatches 197; Indels 0; Gaps 0;  
QY 355 AGATGTACATAGATGATTACCAATATGGGGTATTGTTGGTGAGGCTGATGAAAAATCGAG 414  
Db 4210 ATATATATCTATCTTTATTATCTATATCGCCTGAAAAATCTATTGTTGATTCCTTATAA 4151  
QY 415 AAGATTACTATCTTGGACCTATAAAAAAGTTGAAATAGGTTTTTAATGGAAATCGAATTG 474  
Db 4150 TAAGTTTATTTTATTATATCAATTTTACTTAAACACTCTTTTATTAACCTTTCCCTTTT 4091  
QY 475 TTGATGTTAATCTAAGTAGTGAAGGAAAGTGAAAGTGGTTCCAAATACATAAAATCCAGA 534  
Db 4090 TAATAGTACCATTCTCTATAGATATTTCTTACTTCAATATCAATATTAATATCCATA 4031  
QY 535 TGTCATATTTCAGTAAATGGAAGTCAAGATGTAATTTGAAGATCGATTTGACAAAT 594  
Db 4030 AATCATCTTTAGATAAATTTATATTCGTTGATATGAGATGAAGATAATAATAAAGAGT 3971  
QY 595 ATCTTGATCCGCTCTTTTTCACATCGGATTCATTTGTTCAATTTTTCACATCCTTCA 654  
Db 3970 AGTTCCCTCCTGCTCCATCAATGAATAAGATAAATTTGTTCTTAATTTCTGTAGTAGTTA 3911  
QY 655 TGATGATGATCTCTTTGGTGGCTTAGTTCAATGATTTTAATGAGAACATTA 707  
Db 3910 TAGTTGGCATTAAGAAGTTTCTAGTATCTTATCTAGTTTAAATTTAATATTA 3858

Search completed: January 20, 2003, 16:35:31  
Job time : 356 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2003, 15:42:41 ; Search time 366 Seconds  
(without alignments)  
11075.402 Million cell updates/sec

Title: US-09-319-724A-13  
Perfect score: 1800  
Sequence: 1 ccgcgcgcgtgtgcgtgctg.....gtggaactgtcacagcaaaa 1800

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues 4370478

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_101002.\*  
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.\*  
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.\*  
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1800	100.0	1827	21	AAA08361 Human SM-11044-bin
2	1800	100.0	2072	21	AAA08360 Human SM-11044-bin
3	1794.4	99.7	3370	21	AAA16630 Human secreted pro
4	1753	97.4	3076	22	AAH46951 Human secreted pro
5	1729.6	96.1	2536	22	AAF64216 Human secreted pro
6	1708.4	94.9	2459	22	AAH16543 Human cDNA sequenc
7	1343.4	74.6	2864	22	AAK94275 Human full-length
8	1317	73.2	1317	19	AAV28120 Nucleotide sequenc
9	1104	61.3	2311	22	AAH13994 Human cDNA sequenc

10	1090.4	60.6	2299	22	AAK94454 Human full-length
11	963.4	53.5	965	19	AAV28121 Non-adrenergic SM-
12	743.4	41.3	782	22	AAH05232 Human cDNA clone (
13	716.4	39.8	1070	24	ABL50852 Human polynucleoti
14	696.6	38.7	756	22	AAK92142 Human cDNA 5'-end
15	696.6	38.7	756	22	AAK93404 Human cDNA clone r
16	646	35.9	1863	23	ABLI6691 Drosophila melanog
17	619.6	34.4	1867	22	AAH46935 Human secreted pro
18	604.8	33.6	636	22	AAH07518 Human cDNA clone (
19	576.2	32.0	2060	21	AAK39235 Arabidopsis thalia
20	565.6	31.4	1770	21	AAK42793 Arabidopsis thalia
21	563.6	31.3	4169	23	ABLI6690 Drosophila melanog
22	555.8	30.9	2038	21	AAK48393 Arabidopsis thalia
23	490.2	27.2	661	22	AAH97938 Murine 7-transmemb
24	480	26.7	557	22	AAH97937 Murine 7-transmemb
25	473.6	26.3	489	22	AAK91881 Human cDNA 5'-end
26	473.6	26.3	489	22	AAK93288 Human cDNA clone r
27	455.4	25.3	783	22	AAF94022 Primer specific fo
28	455.4	25.3	1976	22	AAK93822 Human cDNA encodin
29	454	25.2	502	22	AAH97936 Murine 7-transmemb
30	412	22.9	1909	22	AAK94184 Human full-length
31	409.6	22.8	497	24	ABQ58029 Human colon cancer
32	409.4	22.7	418	22	AAK66232 Novel human polynu
33	401	22.3	801	22	AAK91677 Human cDNA 5'-end
34	401	22.3	801	22	AAK93840 Human cDNA clone r
35	387.4	21.5	401	20	AAK40639 Human secreted pro
36	383.4	21.3	440	21	AAK03710 Human secreted pro
37	364.8	20.3	433	21	AAK03504 Human secreted pro
38	360	20.0	600	22	AAK20338 Human breast cance
39	300.8	16.7	731	24	ABK30974 Plant dwarfing/stu
40	285	15.8	285	19	AAV28122 Non-adrenergic SM-
41	282.8	15.7	713	22	AAI94512 Human neuroblastom
42	270.6	15.0	1779	21	AAK43263 Arabidopsis thalia
43	260.4	14.5	2129	21	AAK44903 Arabidopsis thalia
44	248.4	13.8	610	22	AAI11439 Human breast cance
45	238.4	13.2	270	21	AAA44828 Human secreted exp

## ALIGNMENTS

RESULT 1  
AAA08361  
ID AAA08361 standard; cDNA; 1827 BP.  
XX  
AC AAA08361;  
XX  
AC AAA08361;  
DT 30-JUN-2000 (first entry)  
XX  
DE Human SM-11044-binding receptor protein encoding cDNA SEQ ID NO:3.  
DE  
KW Human; SM-11044-binding receptor protein; SMBP; antiasthmatic;  
KW antiinflammatory; inflammation; eosinophil infiltration; asthma;  
KW intestinal disease; eosinophil migration inhibitor; intestinal stress;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 11..1750  
FT FT /\*tag= a  
FT FT /product= "SM-11044-binding receptor protein"  
XX  
XX  
PN WO200014266-A1.  
XX  
PD 16-MAR-2000.  
XX  
PF 06-SEP-1999; 99WO-JP04808.  
XX  
PR 08-SEP-1998; 98JP-0253771.  
XX  
PA (SUMU ) SUMITOMO PHARM CO LTD.  
XX



Db 1698 TGGGAACAAGTGCCTTTGTCCGAAAAATCTATATAATGTGAAATGTGACTAGAGACCCA 1757  
 Qy 1741 AGAAAACTGGAACCTTTGGATCAATTTCTTTTCATAGGGGTGGAACCTTGACACAGCAAAA 1800  
 Db 1758 AGAAAACTGGAACCTTTGGATCAATTTCTTTTCATAGGGGTGGAACCTTGACACAGCAAAA 1817

RESULT 2  
 AAA08360  
 ID AAA08360 standard; cDNA; 2072 BP.  
 AC AAA08360;  
 XX 30-JUN-2000 (first entry)  
 XX Human SM-11044-binding receptor protein encoding cDNA SEQ ID NO:1.  
 DE Human; SM-11044-binding receptor protein; SMBP; antiasthmatic;  
 KW antiinflammatory; inflammation; eosinophil infiltration; asthma;  
 KW intestinal disease; eosinophil migration inhibitor; intestinal stress;  
 KW ss.  
 KW Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH 49..1797  
 FT CDS  
 FT /\*tag= a  
 FT /product= "SM-11044-binding receptor protein"  
 XX W0200014266-A1.  
 PN  
 XX 16-MAR-2000.  
 PD  
 XX 06-SEP-1999; 99WO-JP04808.  
 PF  
 XX 08-SEP-1998; 98JP-0253771.  
 PR  
 XX (SUMI) SUMITOMO PHARM CO LTD.  
 PA Sugasawa T, Hidaka J, Kawakami H;  
 PI WPI; 2000-257008/22.  
 DR P-PSDB; AAY82459.  
 DR  
 XX Recombinant human SM-11044-binding receptor protein with ligand binding  
 PT activity, useful for developing drugs for inflammation accompanying  
 PT eosinophil infiltration, asthma and intestinal diseases -  
 PT  
 PS Claim 2; Page 25-29; 4lpp; Japanese.  
 XX  
 CC The present invention describes transformed cells which express a  
 CC recombinant human SM-11044-binding receptor protein (SMBP) at such  
 CC a high level as to enable the assay of the ligand-binding activity by  
 CC deleting the polythymidine sequence from the base sequence of the  
 CC 3'-nontranslation region or the cell membrane fraction. Also described  
 CC is a method for screening a human SMBP agonist/antagonist characterised  
 CC by using the transformed cells, cell membrane fraction of the  
 CC recombinant human SMBP. The recombinant protein is useful for developing  
 CC drugs for treating inflammation accompanying eosinophil infiltration,  
 CC asthma, and diseases of intestine, particularly agonists as eosinophil  
 CC migration inhibitors or relaxing agents for intestinal stress. The  
 CC protein is easily expressed by transformed cells after deleting  
 CC polythymidine sequence from base sequence of 3'-nontranslation region.  
 CC The present sequence encodes human SMBP from the present invention.  
 XX  
 SQ Sequence 2072 BP; 563 A; 357 C; 461 G; 691 T; 0 other;  
 Query Match 100.0%; Score 1800; DB 21; Length 2072;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGCGCTGTGCTGCTGCTGCCCGGACCCGCGGACGAGCACGAAC 60  
 Db 1145 CCGCGCTTCTTCATCAATTTTCATAGCCCATTTATTACCATGCTTCAAGAGCCATTCCTTTTG 1204

Db 65 CCGCGCGCTGTGCTGCTGCTGCCCGGACCCGCGGACGAGCACGAAC 124  
 Qy 61 ACAGCTATCAGATAAAGAGAAAGTGTCTTTATGATGAATACCTGTTGGGCCCCCTACCATTA 120  
 Db 125 ACAGCTATCAGATAAAGAGAAAGTGTCTTTATGATGAATACCTGTTGGGCCCCCTACCATTA 184  
 Qy 121 ATCGTCAAGAAACATATAAAGTACCTTTTACCTTCCATCTCTGTGTGGGGTCAAAAAAGTA 180  
 Db 185 ATCGTCAAGAAACATATAAAGTACCTTTTACCTTCCATCTCTGTGTGGGGTCAAAAAAGTA 244  
 Qy 181 TCAGTCATTTACCATTGAAACTCTGGGAGAACACCTTCAAGGGTTGAATTTGAATTTAGTG 240  
 Db 245 TCAGTCATTTACCATTGAAACTCTGGGAGAACACCTTCAAGGGTTGAATTTGAATTTAGTG 304  
 Qy 241 GTCGTGATATTAAATTTAAAGATGATGTGATGCCAGCCACTTACTGTGAATTTGATTTAG 300  
 Db 305 GTCGTGATATTAAATTTAAAGATGATGTGATGCCAGCCACTTACTGTGAATTTGATTTAG 364  
 Qy 301 ATAAGAAAAAGAGAGATGCAATTTGTATATGCAATAAAAAATCATTTACTGGTACCAGATGT 360  
 Db 365 ATAAGAAAAAGAGAGATGCAATTTGTATATGCCATAAAAAATCATTTACTGGTACCAGATGT 424  
 Qy 361 ACATAGATGATTTACCAATATGGGGTATTTGTGTGAGGCTGATGAAATTTGAGAGAGATT 420  
 Db 425 ACATAGATGATTTACCAATATGGGGTATTTGTGTGAGGCTGATGAAATTTGAGAGAGATT 484  
 Qy 421 ACTATCTTTGGACCTATAAAAAACTTGAATAGTGTGTTTAAATGGAATTCGAATTTGATG 480  
 Db 485 ACTATCTTTGGACCTATAAAAAACTTGAATAGTGTGTTTAAATGGAATTCGAATTTGATG 544  
 Qy 481 TTAATCTAACTAGTGAAGGAAAGTGAACCTGGTTCCTCAATCTACTTAAATCCAGATGTCAT 540  
 Db 545 TTAATCTAACTAGTGAAGGAAAGTGAACCTGGTTCCTCAATCTACTTAAATCCAGATGTCAT 604  
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 Qy 601 ATCCGTCCTTTTCAACATCGGATTCATTTGGTTTCAATTTTCACTCTCTCATGATGG 660  
 Db 665 ATCCGTCCTTTTCAACATCGGATTCATTTGGTTTCAATTTTCACTCTCTCATGATGG 724  
 Qy 661 TGATCTTCTTTGGTGGCTTAGTTTCAATGATTTTAAATGAGAACAATTAAGAAAAAGATTATG 720  
 Db 725 TGATCTTCTTTGGTGGCTTAGTTTCAATGATTTTAAATGAGAACAATTAAGAAAAAGATTATG 784  
 Qy 721 CTGCGTACAGTAAAGAGAAAGAAATGATGATATGATAGAGAGCTAGGAGATGAATATG 780  
 Db 785 CTGCGTACAGTAAAGAGAAAGAAATGATGATATGATAGAGAGCTAGGAGATGAATATG 844  
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 Db 845 GATGGAACAGGTGCATGGAGATGATTTAGACCATCAAGTCACCCACTGATATTTTCCCT 904  
 Qy 841 CTCTGATTTGGTCTGGATGTGAGATATTTGCTGTGCTCTCTCATGTTATTATTTGTCGAA 900  
 Db 905 CTCTGATTTGGTCTGGATGTGAGATATTTGCTGTGCTCTCTCATGTTATTATTTGTCGAA 964  
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 Qy 961 CTGCTAGCTCTCCAGTCAATGGTTATTTTGGAGGAAGTCTGTATGCTAGACAGGAGGAA 1020  
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 Db 1145 CTGCGTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAGCCATTCCTTTTG 1204



Db	191	TCATTACGATGAACACTCTGGGAGAAGCACTTCAGGGGTGGAATTTAGTGGTCT	240
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Db	241	GGATATTTAAATTTAAAGATGATGTGATGCCAGCCACTTACTCTGAAATTTGATTTAGATAA	300
Qy	305	AGAAAGAGAGATGCATTTGTATATGCCATATAAAATCAATTACTGGTACCAGATGTACAT	364
Db	301	AGAAAGAGAGATGCATTTGTATATGCCATATAAAATCAATTACTGGTACCAGATGTACAT	360
Qy	365	AGATGATTTACCAATATGGGGTATTCGTGGTGAGGCTGATGAAATCGAGAAGATTACTA	424
Db	361	AGATGATTTACCAATATGGGGTATTCGTGGTGAGGCTGATGAAATCGAGAAGATTACTA	420
Qy	425	TCTTTGGACCTATAAAAACTTCGAAATAGGTTTTTAATGGAATCGAATTTGTTGATGTAA	484
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Qy	485	TCTAACTAGTCAGGAAGGTGAACTGGTTCGAAATCTAAATCTCAAGATGTCATATTC	544
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Qy	545	AGTAAATGGAAGAAGTCAGATGTGAATTTGAAGATCGATTGACAAATATCTTGATCC	604
Db	541	AGTAAATGGAAGAAGTCAGATGTGAATTTGAAGATCGATTGACAAATATCTTGATCC	600
Qy	605	GTCCCTTTTTCAACATCGGATTCATTTGGTTTTCAATTTTCAACTCCTTTCATGATGGTGAT	664
Db	601	GTCCCTTTTTCAACATCGGATTCATTTGGTTTTCAATTTTCAACTCCTTTCATGATGGTGAT	660
Qy	665	CTTCTTGGTGGGCTTAGTTTCAATGATTTTAATGAGAACATTAAGAAAAGATTAATGCTCG	724
Db	661	CTTCTTGGTGGGCTTAGTTTCAATGATTTTAATGAGAACATTAAGAAAAGATTAATGCTCG	720
Qy	725	GTACAGTAAAGAGGAAGAAATGATATGATAGAGACCTAGAGATGAATATGGATG	784
Db	721	GTACAGTAAAGAGGAAGAAATGATATGATAGAGACCTAGAGATGAATATGGATG	780
Qy	785	GAACAGGTGCATGGAGATGATTTAGACCATCAAGTCACCCACATGATATTTCTCTCTCT	844
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Qy	845	GATTGGTTCGGATGTCAGATATTTGCTGTGCTCTCATCGTATATTGTTGCAATGAT	904
Db	841	GATTGGTTCGGATGTCAGATATTTGCTGTGCTCTCATCGTATATTGTTGCAATGAT	900
Qy	905	AGAAGATTTATATACTGAGAGGGATCAATGCTCAGTACAGCCATATTGTCATGCTGC	964
Db	901	AGAAGATTTATATACTGAGAGGGATCAATGCTCAGTACAGCCATATTGTCATGCTGC	960
Qy	965	TACGCTCCAGTGAATGGTTATTTTGGAGGAAGTCTGTATGCTAGACAAGGAGGAAGAG	1024
Db	961	TACGCTCCAGTGAATGGTTATTTTGGAGGAAGTCTGTATGCTAGACAAGGAGGAAGAG	1020
Qy	1025	ATGGATTAAGCAGATGTTTATTTGGGGCATTCCTTATPCCAGCATATGTTGTGGCACTGC	1084
Db	1021	ATGGATTAAGCAGATGTTTATTTGGGGCATTCCTTATPCCAGCATATGTTGTGGCACTGC	1080
Qy	1085	CTTCTTCATCAATTTTCATAGCCATTTTACCATGCTTCAAGGCCATTCCTTTTGAAC	1144
Db	1081	CTTCTTCATCAATTTTTCATAGCCATTTTACCATGCTTCAAGGCCATTCCTTTTGAAC	1140
Qy	1145	AATGGTGGCGTGTGTGCACTGTTTTTTTGTATCTTCTCTCTAAATCTGTTGGTAC	1204
Db	1141	AATGGTGGCGTGTGTGCACTGTTTTTTTGTATCTTCTCTCTAAATCTGTTGGTAC	1200
Qy	1205	AATACTTTGGCCGAATCTGTCAAGTTCAGCCCAACTTTTCTTCTGCTGTCAATGCTGTGCC	1264
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Qy	1265	TCGTCTTATACCGGAGAAAATATGTTTCATGAGGCTCGGGTTATTTGTTGCGTGGGTGG	1324
Db	1261	TCGTCTTATACCGGAGAAAATATGTTTCATGAGGCTCGGGTTATTTGTTGCGTGGGTGG	1320

## RESULT 4

AAH46951

ID	AAH46951	standard	cdNA	3076 BP

AAH46951;

DT 25-SEP-2001 (first entry)

Human secreted protein encoding cDNA (clone Id HBOEG11).

Secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
nootropic; neuroprotective; antibacterial; virucide; fungicide; human;  
ophthalmological; gene therapy; ss.

Homo sapiens.

PN WO200155430-A1.

XX PD 02-AUG-2001

17-JAN-2001: 2001WO-US01431.

XX  
PR 31-JAN-2000: 2000US-0179065

PR 04-FEB-2000; 2000US-0180628.

PR 12-SEP-2000; 2000US-0231968.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;  
PI Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;  
PI Moore PA, Duan DR, Shi Y, Choi GH, Fiscella M;

FI NI U, RUDELL SM, BR  
XX

DR WPI; 2001-476220/

17 isolated nucleic acid molecules encoding human secreted proteins, used to preventing, treating or ameliorating a medical condition -

XX

Claim 1; page 426-427; 482pp; English.

The invention provides novel human secreted proteins and polynucleotides encoding them. The secreted proteins can be expressed by standard recombinant methodology. The secreted proteins and polynucleotides are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can also be used in diagnosing a pathological condition. The antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a human secreted protein encoding cDNA.

Sequence 3076 BP; 940 A; 487 C; 617 G; 1028 T; 4 other;

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Query Match          97.4%; Score 1753; DB 22; Length 3076;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 1762; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
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Qy	18	CTGCTGCTGCTGCTGCCCCCGGAGCCCGGGCCGAGCAGCAGCAACACACACAGTATCAAGATAA	77
Db	13	CTGCAGGTACCGGTCCGGAAATCCCGGGTCGAGSCAGCGGCMGCGACGTATCAAGATAA	72
Qy	78	GAGCAAGTTGTCTTATCGATCAATACHTGTTGGCCCTACCATAATCGTCAAGAAACATAT	137
Db	73	GAGCAAGTTGTCTTATCGATGAATACHTGTTGGCCCTACCATAATCGTCAAGAAACATAT	132
Qy	138	AAGTACTTTTTCACCTTCATTTCTGTGTGGGGTCAAAAAAAGTATCATGTACATTTACCATGAA	197
Db	133	AAGTACTTTTTCACCTTCATTTCTGTGTGGGGTCAAAAAAAGTATCATGTACATTTACCATGAA	192
Qy	198	ACTCTGGGAGAGCACATTCAGGGGTGAATGGAATTTAGTGGTCTGGATATTAATTTT	257
Db	193	ACTCTGGGAGAGCACATTCAGGGGTGAATGGAATTTAGTGGTCTGGATATTAATTTT	252
Qy	258	AAAGATGATGTGATGCCAGCCACTTACTGTGAAATTTGATTTAGATAAAGAAAGACAGAT	317
Db	253	AAAGATGATGTGATGCCAGCCACTTACTGTGAAATTTGATTTAGATAAAGAAAGACAGAT	312
Qy	318	GCATTTGTATATGCCATPAAAAATCAATTACTGCTACCAGATGTACATAGATGATTTTACCA	377
Db	313	GCATTTGTATATGCCATPAAAAATCAATTACTGCTACCAGATGTACATAGATGATTTTACCA	372
Qy	378	ATATGGGGTATTTCTGTGAGGCTGATGAAATTTGGAGAGATTACTATCTTTGGACCTAT	437
Db	373	ATATGGGGTATTTCTGTGAGGCTGATGAAATTTGGAGAGATTACTATCTTTGGACCTAT	432
Qy	438	AAAAAATCTGAAATAGTTTTTAATGGAAATTCGAATTTGTATCTTAATCTAACTAGTGA	497
Db	433	AAAAAATCTGAAATAGTTTTTAATGGAAATTCGAATTTGTATCTTAATCTAACTAGTGA	492
Qy	498	GGAAAGGTGAACTGGTTCCAAATCTAAATCCAGATGTCAATATTCAGTAAAAATGGAAA	557
Db	493	GGAAAGGTGAACTGGTTCCAAATCTAAATCCAGATGTCAATATTCAGTAAAAATGGAAA	552
Qy	558	AAGTCAGATCTGAAATTTGAAGATCGATTTGACAAATATCTTGTGATCCGTCCTTTTTCAA	617
Db	553	AAGTCAGATCTGAAATTTGAAGATCGATTTGACAAATATCTTGTGATCCGTCCTTTTTCAA	612
Qy	618	CATCGGAATTCATTTGGTTTTTCAATTTTCAACTCCCTTCATGATGGTGATCTCTTGGTGGCG	677
Db	613	CATCGGAATTCATTTGGTTTTTCAATTTTCAACTCCCTTCATGATGGTGATCTCTTGGTGGCG	672



Qy 1758 GGATCAATTTCTTTTCATAGGGTGGAACTTGACAGCAAAA 1800  
Db 1753 GGATCAATTTCTTTTCATAGGGTGGAACTTGACAGCAAAA 1795

RESULT 5  
AAF64216  
ID AAF64216 standard; cDNA; 2536 BP.

XX AAF64216;  
XX  
XX  
XX 06-APR-2001 (first entry)  
DE Human secreted protein gene 41 SEQ ID NO:51.

XX Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW neotropic; neuroprotective; antibacterial; virucide; fungicide;  
KW ophthalmological; vulnerary; autoimmune disease; cardiovascular disorder;  
KW hyperproliferative disorders; cerebrovascular disorder; wound healing;  
KW nervous system disorder; ocular disorder; skin ageing; chemotaxis;  
KW food additive; ss.

XX Homo sapiens.  
OS  
XX WO200077026-A1.  
XX  
XX 21-DEC-2000.

XX 01-JUN-2000; 2000WO-US14973.  
XX  
XX 11-JUN-1999; 99US-0138630.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX (ROSE/) ROSEN C A.

XX Rosen CA, Ruben SM, Komatsoulis GA;  
PI WPI: 2001-071258/08.  
XX P-PSDB; AAB75546.  
DR  
DR  
XX

XX Nucleic acid molecules encoding human secreted proteins, used in  
PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and  
PT Parkinson's diseases and cancers -

XX Claim 1; Page 462-463; 542pp; English.

XX Human secreted proteins AAB75506 - AAB75554 are encoded by polynucleotide  
CC sequences AAF64176 - AAF64224. The specification includes amino acid  
CC sequences AAB75555 - AAB75606 which represent fragments of the human  
CC secreted proteins, and protein sequences with which they share homology.  
CC The proteins and polynucleotides, their agonists and antagonists have  
CC activities dependent on the tissues and cells in which they are  
CC expressed, examples of these activities include, immunosuppressive;  
CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;  
CC vasotropic; cerebroprotective; neotropic; neuroprotective; antibacterial;  
CC virucide; fungicide; ophthalmological; and vulnerary. The proteins,  
CC polynucleotides, agonists and antagonists can be used to treat or detect  
CC or diagnose various diseases and disorders including, autoimmune  
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders  
CC e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
CC infections caused by bacteria, viruses and fungi and ocular disorders  
CC e.g. corneal infection. The polypeptides can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin ageing due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities. Included in the invention are  
CC polynucleotide sequences AAF64167 - AAF64175 and peptide AAB75505 which  
CC are used in the isolation, identification and characterisation of the  
CC proteins of the invention.

D	b	964		AGGAGGAAGGAGATGGATATAAAGCAGATGTTTATTGGGGCATTCCTTATCCCGACGTATGGT	1023
Q	y	1073		GTGTGGCAC TGCCCTTCATCAATTTCAATFAGCCATTTATTACCATGCCTCAAAGAGCCAT       	1132
D	b	1024		GTGTGGCAC TGCCCTTCATCAATTTCAATAGCCATTTATTACCATGCCTCAAAGAGCCAT	1083
Q	y	1133		TCCTTTTTGGAACAATGGTGCCCGTTGTGTGCCATCTGCTTTTTTTTGTATTCTTCCCTCTAAA       	1192
D	b	1084		TCCTTTTTGGAACAATGGTGCCCGTTGTGTGCCATCTGCTTTTTTTTGTATTCTTCCCTCTAAA	1143
Q	y	1193		TC TT GT TGGT ACA ATACT TC GG CG GA AAT CT GC AG GT CA G CC CAA CTC TT CCT GT G C GT GT       	1252
D	b	1144		TC TT GT TGGT ACA ATACT TC GG CG GA AAT CT GC AG GT CA G CC CAA CTC TT CCT GT G C GT GT       	1203
Q	y	1253		CAATGCCTGCGCCCTGCCTATACCGGAGAAAAATGGTTTCATGGAGCCTGCGGTTATTGT       	1312
D	b	1204		CAATGCCTGCGCCCTGCCTATACCGGAGAAAAATGGTTTCATGGAGCCTGCGGTTATTGT       	1263
Q	y	1313		TTGCCTGGGTGGAATTTTACCTTTTGGTTCAACTCTTATTGAAATGTATTTTCATCTTCAC       	1372
D	b	1264		TTGCCTGGGTGGAATTTTACCTTTTGGTTCAACTCTTATTGAAATGTATTTTCATCTTCAC	1323
Q	y	1373		GTC TT CT GGG CAT ATAAGA TCT ATT AT GT CTA TGG CTT CAT GTA GCT GGT GCT GT GT AT       	1432
D	b	1324		GTC TT CT GGG CAT ATAAGA TCT ATT AT GT CTA TGG CTT CAT GTA GCT GGT GCT GT AT       	1383
Q	y	1433		CCTGTGCATTTGTGACTGCTCTGTGACTATTGTGTGCACATATTTTCTACTAAATGCAGA       	1492
D	b	1384		CTGTGCATTTGTGACTGCTGTGACTATTGTGTGCACATATTTTCTACTAAATGCAGA	1443
Q	y	1493		AGATTACCGGTGGCAATGGACAAGTTTTCTCTCTGTGCATCACTGCAATCTATGTTTA       	1552
D	b	1444		AGATTACCGGTGGCAATGGACAAGTTTTCTCTCTGTGCATCACTGCAATCTATGTTTA	1503
Q	y	1553		CATGTATTCCTTTTACTACTATATTTTTTCAAACAAGATGTATGGCTTATTTCAAACAATC       	1612
D	b	1504		CATGTATTCCTTTTACTACTATATTTTTTCAAACAAGATGTATGGCTTATTTCAAACAATC	1563
Q	y	1613		ATTTTACTTTTGGATATATGCGGTATTTAGCACAGCCTTGGGGATAATGCTGGAGCGAT       	1672
D	b	1564		ATTTTACTTTTGGATATATGCGGTATTTAGCACAGCCTTGGGGATAATGCTGGAGCGAT	1623
Q	y	1673		TGGTTACATGGGAACAAGTGCCCTTTCTCCGAAAAATCTATACTAATGTGAAAAATTGACTA       	1732
D	b	1624		TGGTTACATGGGAACAAGTGCCCTTTCTCCGAAAAATCTATACTAATGTGAAAAATTGACTA	1683
Q	y	1733		GAGACCCAAGAACCTCGAACCTTTGGATCAATTTCTTTTTTCATAGGGGTGGAACCTTGCA       	1792
D	b	1684		GAGACCCAAGAACCTCGAACCTTTGGATCAATTTCTTTTTTCATAGGGGTGGAACCTTGCA	1743
Q	y	1793		CAGCAAAA 1800 	
D	b	1744		CAGCAAAA 1751 	
RESULT 6					
AAH16543					
I	d	AAH16543	standard; cDNA; 2459 BP.		
X	x	XX	AC	AAH16543;	
X	x	XX	AC		
D	t	DT	(first entry)		
X	x	XX			
D	E	DE	Human cDNA sequence SEQ ID NO:15599.		
X	x	XX	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.		
X	x	XX	Homo sapiens.		
O	S	OS			
P	N	PN	EP1074617-A2.		
X	x	XX			
P	D	PD	07-FEB-2001.		
X	x	XX			

PF	28-JUL-2000;	2000EP-0116126.	
XX			
PR	29-JUL-1999;	99JP-0248036.	
PR	27-AUG-1999;	99JP-0300253.	
PR	11-JAN-2000;	2000JP-0118776.	
PR	02-MAY-2000;	2000JP-0183767.	
PR	09-JUN-2000;	2000JP-0241899.	
XX			
PA	(HELI-) HELIX RES INST.		
XX			
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;		
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;		
XX			
DR	WPI; 2001-318749/34.		
XX			
PT	Primer sets for synthesizing polynucleotides, particularly the 5602		
PT	full-length cDNAs defined in the specification, and for the detection		
PT	and/or diagnosis of the abnormality of the proteins encoded by the		
PT	full-length cDNAs -		
XX			
PS	Claim 8; SEQ ID 15599; 2537pp + CD ROM; English.		
XX			
CC	The present invention describes primer sets for synthesizing 5602		
CC	full-length cDNAs defined in the specification. Where a primer set		
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary		
CC	to the complementary strand of a polynucleotide which comprises one of		
CC	the 5602 nucleotide sequences defined in the specification, where the		
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination		
CC	of an oligonucleotide comprising a sequence complementary to the		
CC	complementary strand of a polynucleotide which comprises a 5'-end		
CC	sequence and an oligonucleotide comprising a sequence complementary to a		
CC	polynucleotide which comprises a 3'-end sequence, where the		
CC	oligonucleotide comprises at least 15 nucleotides and the combination of		
CC	the 5'-end sequence/3'-end sequence is selected from those defined in		
CC	the specification. The primer sets can be used in antisense therapy and		
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,		
CC	particularly full-length cDNAs. The primers are also useful for the		
CC	detection and/or diagnosis of the abnormality of the proteins encoded by		
CC	the full-length cDNAs. The primers allow obtaining of the full-length		
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and		
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB992446 to		
CC	AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632		
CC	represent oligonucleotides, all of which are used in the exemplification		
CC	of the present invention.		
XX			
SQ	Sequence 2459 BP; 728 A; 399 C; 490 G; 842 T; 0 other;		
	Query Match	94.9%;	Score 1708.4; DB 22; Length 2459;
	Best Local Similarity	99.9%;	Pred. No. 0;
	Matches 1709; Conservative	0; Mismatches	1; Indels 0; Gaps 0
QY	91	TATGGATGAATACTGTGGGCCCTACCATAATCGTCAAGAACATATAAGTACTTTTCAC	150
DB	1	TATGGATGAATACTGTGGGCCCTACCATAATCGTCAAGAACATATAAGTACTTTTCAC	60
QY	151	TTCCATTCTGTGGGGTCAAAAAAGATATCAGTCATTCACATCAACACTCGGAGAAG	210
DB	61	TTCCATTCTGTGGGGTCAAAAAAGATATCAGTCATTCACATCAACACTCGGAGAAG	120
QY	211	CACCTTCAAGGGTGTGAATTTGGAATTTAGTGGTCTGGATATTAATTTAAAGATGATGTGA	270
DB	121	CACCTTCAAGGGTGTGAATTTGGAATTTAGTGGTCTGGATATTAATTTAAAGATGATGTGA	180
QY	271	TGCCAGCCACTTACTGTGAAATTTAGATTAAGAAAAGAGAGATGCATTTGTATATG	330
DB	181	TGCCAGCCACTTACTGTGAAATTTAGATTAAGAAAAGAGAGATGCATTTGTATATG	240
QY	331	CCATAAAAAATCATTTACTTGGTACCAGATGTCATAGATGATTTTACCATAATGGGGTATTG	390
DB	241	CCATAAAAAATCATTTACTTGGTACCAGATGTCATAGATGATTTTACCATAATGGGGTATTG	300
QY	391	TTGGTGCAGGCTGATGAAATGGAGAAGATTACTATCTTTGGACCTATAAAAACTTGAAA	450

Db 301 TTGGTGAGGCTGTAGAAATGGAGAGATTACTATCTTTGGACCTATAAAAAAAGCTTGAAA 360  
Qy 451 TAGGTTTTTAATGGAATCGAATCTTGTATGTTAACTAAGTGTAGTGAAGGAAAGGTGAAC 510  
Db 361 TAGGTTTTTAATGGAATCGAATCTTGTATGTTAACTAAGTGTAGTGAAGGAAAGGTGAAC 420  
Qy 511 TGGTTCGAATACTAAATCCAGATGTCATATTCAGTAAATGGAAGGAAAGGTGATGTA 570  
Db 421 TGGTTCGAATACTAAATCCAGATGTCATATTCAGTAAATGGAAGGAAAGGTGATGTA 480  
Qy 571 AATTGGAAGATCGATTTGACAATATCTTGCATCGTCCCTTTTTCACATCGGATTCATT 630  
Db 481 AATTGGAAGATCGATTTGACAATATCTTGCATCGTCCCTTTTTCACATCGGATTCATT 540  
Qy 631 GGTGTTTCAATTTTCAACTCTTCATGATGGTGTATCTTCTGGTGGGCTAGTTTCAATGA 690  
Db 541 GGTGTTTCAATTTTCAACTCTTCATGATGGTGTATCTTCTGGTGGGCTAGTTTCAATGA 600  
Qy 691 TTTTAATGAGAATTAAGAAAGATATGCTCGGTACAGTAAAGAGAAAGAAATGGATG 750  
Db 601 TTTTAATGAGAATTAAGAAAGATATGCTCGGTACAGTAAAGAGAAAGAAATGGATG 660  
Qy 751 ATATGGATAGACCTAGGAGATGAATATGATGGAGAAACAGGTGCATGGAGATGATTTA 810  
Db 661 ATATGGATAGACCTAGGAGATGAATATGATGGAGAAACAGGTGCATGGAGATGATTTA 720  
Qy 811 GACCATCAAGTCACCCACTGATATTTTCCCTCTGATTTGTTCTGGATGTCAGATATTG 870  
Db 721 GACCATCAAGTCACCCACTGATATTTTCCCTCTGATTTGTTCTGGATGTCAGATATTG 780  
Qy 871 CTGTGCTCTCATCGTTTATTATGTTGCAATGATAGAGATTTATATACCTAGAGGGGAT 930  
Db 781 CTGTGCTCTCATCGTTTATTATGTTGCAATGATAGAGATTTATATACCTAGAGGGGAT 840  
Qy 931 CAATGCTCAGTACAGCCATATTTGCTCTGCTAGTCTCCAGTCAATGGTTATTG 990  
Db 841 CAATGCTCAGTACAGCCATATTTGCTCTGCTAGTCTCCAGTCAATGGTTATTG 900  
Qy 991 GAGGAAGTCTGTATGCTAGCAAGGAGAGAGATGGATAAAGCAGATGTTTATTTGGG 1050  
Db 901 GAGGAAGTCTGTATGCTAGCAAGGAGAGAGATGGATAAAGCAGATGTTTATTTGGG 960  
Qy 1051 CATTCTTATCCAGCTATGGTGTGGCAGTGCCTTCTTCATCAATTTTCATAGCCATTT 1110  
Db 961 CATTCTTATCCAGCTATGGTGTGGCAGTGCCTTCTTCATCAATTTTCATAGCCATTT 1020  
Qy 1111 'ATTACCATGCTTCAAGAGCCATTCCTTTTGGAAACAATGGTGGCGTTTGTGCATCTGTT 1170  
Db 1021 ATTACCATGCTTCAAGAGCCATTCCTTTTGGAAACAATGGTGGCGTTTGTGCATCTGTT 1080  
Qy 1171 TTTTGTGTTATTTCTCCCTCTAAATCTTCTGTTACAAATCTTGGCGGAAATCTGTGAGGTC 1230  
Db 1081 TTTTGTGTTATTTCTCCCTCTAAATCTTCTGTTACAAATCTTGGCGGAAATCTGTGAGGTC 1140  
Qy 1231 AGCCCAACTTTCCCTGTGCTCAATGCTGCTCTCTATACCGGAGGAAATGGT 1290  
Db 1141 AGCCCAACTTTCCCTGTGCTCAATGCTGCTCTCTATACCGGAGGAAATGGT 1200  
Qy 1291 TCATGGAGCCTCGGTTATTGTTGCTGCTGGTGGAAATTTTACCTTTTGGTTCAATCTTTA 1350  
Db 1201 TCATGGAGCCTCGGTTATTGTTGCTGCTGGTGGAAATTTTACCTTTTGGTTCAATCTTTA 1260  
Qy 1351 TTGAATGTTATTTCAATCTTCCAGTCTTCTGCGGATATAAGATCTATTATCTCTATGCT 1410  
Db 1261 TTGAATGTTATTTCAATCTTCCAGTCTTCTGCGGATATAAGATCTATTATCTCTATGCT 1320  
Qy 1411 TCATGATGCTGGTCTGTTTATCTCTGCAATGTGACTGTCTGTGACTATTGTGTGCA 1470  
Db 1321 TCATGATGCTGGTCTGTTTATCTCTGCAATGTGACTGTCTGTGACTATTGTGTGCA 1380  
Qy 1471 CATATTTTCTACTAAATGCAGAGATTACCGGTGGCAATGGCAAGTTTCTCTCTGCTG 1530  
Db 1381 CATATTTTCTACTAAATGCAGAGATTACCGGTGGCAATGGCAAGTTTCTCTCTGCTG 1440

Qy 1531 CATCAACTGCAATCTATGTTTACATGTATCCCTTTTACTACTATTTTTCAAAAACAAGA 1590  
Db 1441 CATCAACTGCAATCTATGTTTACATGTATCCCTTTTACTACTATTTTTCAAAAACAAGA 1500  
Qy 1591 TGTATGCTTATTTTCAAAACATCATTTTACATTTTGGATATATGGCGGTATTTAGCACAGCCT 1650  
Db 1501 TGTATGCTTATTTTCAAAACATCATTTTACATTTTGGATATATGGCGGTATTTAGCACAGCCT 1560  
Qy 1651 TGGGATAAATGCTGGAGCGATTGTTACATGGGAACAAGTGCCTTTGTCGAAAAATCT 1710  
Db 1561 TGGGATAAATGCTGGAGCGATTGTTACATGGGAACAAGTGCCTTTGTCGAAAAATCT 1620  
Qy 1711 ATACTAATGTGAAAATTTGACTAGAGACCCCAAGAAAAACCTTGGATCAATTTTCTT 1770  
Db 1621 ATACTAATGTGAAAATTTGACTAGAGACCCCAAGAAAAACCTTGGATCAATTTTCTT 1680  
Qy 1771 TTTTCATAGGGGTGGAACCTTGCACAGCAAAA 1800  
Db 1681 TTTTCATAGGGGTGGAACCTTGCACAGCAAAA 1710

RESULT 7  
AAK94275  
ID AAK94275 standard; cDNA; 2864 BP.  
XX AAK94275;  
XX AC AC  
XX 06-NOV-2001 (first entry)  
DT  
XX  
DE Human full-length cDNA, SEQ ID NO: 2908.  
DE  
XX  
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
KW  
XX Homo sapiens.  
XX  
PN EP1130094-A2.  
XX  
XX 05-SEP-2001.  
XX  
XX 07-JUL-2000; 2000EP-0114089.  
XX  
XX 08-JUL-1999; 99JP-0194486.  
PR 11-JAN-2000; 2000JP-0118774.  
PR 02-MAY-2000; 2000JP-0183765.  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
DR WPI; 2001-524255/58.  
DR P-PSDB; AAM93355.  
XX

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation -

Claim 8; SEQ ID NO 2908; 1380pp + sequence listing; English.

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.

Sequence 2864 BP; 834 A; 463 C; 569 G; 998 T; 0 other;

Query Match		74.6%;	Score 1343.4;	DB 22;	Length 2864;		
Best Local Similarity		99.9%;	Pred. No. 0;				
Matches 1344;		Conservative	0;	Mismatches	1;	Indels	0; Gaps
		0;					
QY	456	TTTAAAGGAATCGAATTTGTTGATGTTAACTAAGTGAAGAAAGGTGAAACTGGTT	515				
DB	1	TTTAAAGGAATCGAATTTGTTGATGTTAACTAAGTGAAGAAAGGTGAAACTGGTT	60				
QY	516	CCAAATACATAAATCCAGATGTCATATTCAGTAAATGGAAAGTCAGATGTGAATTT	575				
DB	61	CCAAATACATAAATCCAGATGTCATATTCAGTAAATGGAAAGTCAGATGTGAATTT	120				
QY	576	GAAGATCGAATTTGACAAATATCTTGATCCGTCCTTTTCAACATCGGATTCATTCGGTT	635				
DB	121	GAAGATCGAATTTGACAAATATCTTGATCCGTCCTTTTCAACATCGGATTCATTCGGTT	180				
QY	636	TCAATTTTCAACTCCCTCATGATGGTGATCTTCTTGGTGGGCTTAGTTCAATGATTTTA	695				
DB	181	TCAATTTTCAACTCCCTCATGATGGTGATCTTCTTGGTGGGCTTAGTTCAATGATTTTA	240				
QY	696	ATCAGAACATTAAAGAAAGATTATGCTCCGTACAGTAAAGAGGAAGAAATGGATGATG	755				
DB	241	ATCAGAACATTAAAGAAAGATTATGCTCCGTACAGTAAAGAGGAAGAAATGGATGATG	300				
QY	756	GATAGAGACCTAGGAGATGAATATGGATGGAACAGGTGCATGGAGATGTATTTAGACCA	815				
DB	301	GATAGAGACCTAGGAGATGAATATGGATGGAACAGGTGCATGGAGATGTATTTAGACCA	360				
QY	816	TCAAGTACCCACTGATATTTTCCCTCTCTGATTTGGTCTGGATGTCAGATATTTGCTGTG	875				
DB	361	TCAAGTACCCACTGATATTTTCCCTCTCTGATTTGGTCTGGATGTCAGATATTTGCTGTG	420				
QY	876	TCCTCATCGTTATTTGTTGCAATGATAGAAATTTATATACTCAGAGGGGATCAATG	935				
DB	421	TCCTCATCGTTATTTGTTGCAATGATAGAAATTTATATACTCAGAGGGGATCAATG	480				
QY	936	CTCAGTACAGCCATATTTGCTATGCTGCTACGCTCCAGTGAATGTTATTTGGAGGA	995				
DB	481	CTCAGTACAGCCATATTTGCTATGCTGCTACGCTCCAGTGAATGTTATTTGGAGGA	540				
QY	996	AGTCTGTATGCTACAGAGGAGGAGATGGATGAAGACAGATGTTATTTGGGGCATTC	1055				
DB	541	AGTCTGTATGCTACAGAGGAGGAGATGGATGAAGACAGATGTTATTTGGGGCATTC	600				
QY	1056	CTTATCCACGCTATGTTGTCGCTGCTGCTCTTCTTCAATTCATAGCCATTTATTAC	1115				
DB	601	CTTATCCACGCTATGTTGTCGCTGCTGCTCTTCTTCAATTCATAGCCATTTATTAC	660				
QY	1116	CATGCTTCAAGAGCCATTTCTTTTGGAAACAAATGGTGGCGTTTGTGGCATCTGTTTTTT	1175				
DB	661	CATGCTTCAAGAGCCATTTCTTTTGGAAACAAATGGTGGCGTTTGTGGCATCTGTTTTTT	720				
QY	1176	GTTATTTCTTCTTAATCTTTGTTGGTACAAATCTTGGCGAAATCTGTCAGGTCAGCCC	1235				
DB	721	GTTATTTCTTCTTAATCTTTGTTGGTACAAATCTTGGCGAAATCTGTCAGGTCAGCCC	780				
QY	1236	AACCTTTCTTGTGTCATGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1295				
DB	781	AACCTTTCTTGTGTCATGCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840				
QY	1296	GAGCCTGCGGTTATTTCTTGGCTGGGCTGGAATTTTACCTTTTGGTTCAATCTTTATTGAA	1355				
DB	841	GAGCCTGCGGTTATTTCTTGGCTGGGCTGGAATTTTACCTTTTGGTTCAATCTTTATTGAA	900				
QY	1356	ATGATTTTCAATCTACAGCTTTTCTGGGCATATAAGATCTATTAATGCTATGCTTCATG	1415				
DB	901	ATGATTTTCAATCTACAGCTTTTCTGGGCATATAAGATCTATTAATGCTATGCTTCATG	960				
QY	1416	ATGCTGGTGGTTCATCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1475				
DB	961	ATGCTGGTGGTTCATCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1020				

QY	1476	TTTCTACTAAATGACAGAGATTACCGTGGCAATGACAAAGTTTCTCTCTGCTGCATCA	1535
DB	1021	TTTCTACTAAATGACAGAGATTACCGTGGCAATGACAAAGTTTCTCTCTGCTGCATCA	1080
QY	1536	ACTGCAATCTATGTTTACATGATTCCTTTTACTACTATTTTTCACAAACAAGATGTAT	1595
DB	1081	ACTGCAATCTATGTTTACATGATTCCTTTTACTACTATTTTTCACAAACAAGATGTAT	1140
QY	1596	GGCTTATTTCAACATCATTTTACTTTGGATATATGCGGTATTTAGCACAGCCTTGGGG	1655
DB	1141	GGCTTATTTCAACATCATTTTACTTTGGATATATGCGGTATTTAGCACAGCCTTGGGG	1200
QY	1656	ATAATGTGTGGAGCGATTGTTACATGGGAACAAGTCCCTTTGTCGAAAAATCTATACT	1715
DB	1201	ATAATGTGTGGAGCGATTGTTACATGGGAACAAGTCCCTTTGTCGAAAAATCTATACT	1260
QY	1716	AATGTGAAATTTGACTAGAGACCCCAAGAAACCTTGAACCTTTGGATCAATTTCTTTTCA	1775
DB	1261	AATGTGAAATTTGACTAGAGACCCCAAGAAACCTTGAACCTTTGGATCAATTTCTTTTCA	1320
QY	1776	TAGGGGTGGAACCTTGCACAGCAAAA	1800
DB	1321	TAGGGGTGGAACCTTGCACAGCAAAA	1345
RESULT 8			
AAV28120			
ID	AAV28120 standard: cDNA; 1317 BP.		
XX	AC AAV28120;		
XX	DT 25-SEP-1998 (first entry)		
XX	DE Nucleotide sequence encoding non-adrenergic SM-binding protein.		
XX	KW Non-adrenergic SM binding protein; human; muscle; receptor; ss;		
XX	KW Iodocyanopindolol.		
XX	OS Homo sapiens.		
FH	Key Location/Qualifiers		
FT	CDS 1..1317		
FT	/*tag= a		
FT	/product= "non-adrenergic SM-binding protein"		
XX	EP848059-A1.		
XX	17-JUN-1998.		
XX	12-DEC-1996; 96EP-0402719.		
XX	12-DEC-1996; 96EP-0402719.		
XX	(VETI-) VETIGEN.		
XX	Lenzen G, Morooka S, Strosberg AD, Sugasawa T;		
XX	WPI: 1998-314474/28.		
DR	P-PSDB; AAW61371.		
XX	New iodocyanopindolol receptor polypeptide - and corresponding DNA,		
PT	antibodies, etc.		
PS	Claim 4; Page 22-23; 56pp; English.		
CC	The non-adrenergic SM binding protein is found in human muscles. It is		
CC	a member of a novel receptor class which have a receptor activity other		
CC	than that of beta3-adrenergic receptors. The protein comprises sites		
CC	which, when exposed on the cell surface, are capable of binding		
CC	iodocyanopindolol (ICYP) under blockade of alpha , beta 1, beta 2 and		
CC	beta 3 adrenergic receptors and serotonin 5-HT1A and 5-HT1B receptors.		
CC	The binding is saturable and reversible by displacement with the		
CC	stereoselective beta-adrenergic receptor agonist SM-11044 but not		

CC	isoproterenol, epinephrine, norepinephrine, serotonin, dopamine or
XX	BRL-37344.
SQ	Sequence 1317 BP; 355 A; 211 C; 288 G; 463 T; 0 other;
Query Match 73.2%; Score 1317; DB 19; Length 1317;	
Best Local Similarity 100.0%; Pred. No. 0;	
Matches 1317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	357 ATGTACATAGATATTTACCAATATGGGTATTTGCTGAGCTGATGAAATGGAGAA 416
Db	
QY	1 ATGTACATAGATATTTACCAATATGGGTATTTGCTGAGCTGATGAAATGGAGAA 60
Db	
QY	417 GATTACTATCTTTGGACCTATAAAAACTTGAATAGTGTTTAATGAAAAATCGAATGTT 476
Db	
QY	61 GATTACTATCTTTGGACCTATAAAAACTTGAATAGTGTTTAATGAAAAATCGAATGTT 120
Db	
QY	477 GATGTTAATCTAAGTGAAGAAAGGTGAAACTGGTTCCTCAATACTAAAATCCAGATG 536
Db	
QY	121 GATGTTAATCTAAGTGAAGAAAGGTGAAACTGGTTCCTCAATACTAAAATCCAGATG 180
Db	
QY	537 TCATATTCACTAAAATGGAAGAGTCAAGATCTGAAATTTTCAAGATCGATTTGACAAATAT 596
Db	
QY	181 TCATATTCACTAAAATGGAAGAGTCAAGATCTGAAATTTTCAAGATCGATTTGACAAATAT 240
Db	
QY	597 CTTGATCCGTCCTTTTCAACATCGGATTCATTTGTTTCAATTTTCAACTCCTTCATG 656
Db	
QY	241 CTTGATCCGTCCTTTTCAACATCGGATTCATTTGTTTCAATTTTCAACTCCTTCATG 300
Db	
QY	657 ATGGTATCTCTTGGTGGCTTAGTTTCAATGATTTTAATGAGAACATTAAGAAAGAT 716
Db	
QY	301 ATGGTATCTCTTGGTGGCTTAGTTTCAATGATTTTAATGAGAACATTAAGAAAGAT 360
Db	
QY	717 TATGCTCGGTACAGTAAAGAGGAGAAATGGATGATATGGATAGAGACCTAGGAGATGAA 776
Db	
QY	361 TATGCTCGGTACAGTAAAGAGGAGAAATGGATGATATGGATAGAGACCTAGGAGATGAA 420
Db	
QY	777 TATGGATGGAACAGGTGCATGGAGATGATTTAGACCATCAAGTACCACCTGATATTT 836
Db	
QY	421 TATGGATGGAACAGGTGCATGGAGATGATTTAGACCATCAAGTACCACCTGATATTT 480
Db	
QY	837 TCCTCTCTGATGGTCTCGAGTGCAGATATTTGCTGTCTCTCATCGTATATTTGTT 896
Db	
QY	481 TCCTCTCTGATGGTCTCGAGTGCAGATATTTGCTGTCTCTCATCGTATATTTGTT 540
Db	
QY	897 GCAATGATAGCAATTTATATCTGAGAGGGATCAATGCTCAGTACAGCCATTTTGTG 956
Db	
QY	541 GCAATGATAGCAATTTATATCTGAGAGGGATCAATGCTCAGTACAGCCATTTTGTG 600
Db	
QY	957 TATGCTGCTACGTCCTCAGTGAATGGTTATTTTGGAGGAAGTCTGTATGCTAGACAAGGA 1016
Db	
QY	601 TATGCTGCTACGTCCTCAGTGAATGGTTATTTTGGAGGAAGTCTGTATGCTAGACAAGGA 660
Db	
QY	1017 GGAAGGAGATGGATAAGCAGATGTTTATTTGGGGCATTCCTTATCCAGCATATGGTGTG 1076
Db	
QY	661 GGAAGGAGATGGATAAGCAGATGTTTATTTGGGGCATTCCTTATCCAGCATATGGTGTG 720
Db	
QY	1077 GGCACCTGCTTCTCATCAATTTTCAAGCCATTTATACCATGCTTCAAGAGCCATTCCT 1136
Db	
QY	721 GGCACCTGCTTCTCATCAATTTTCAAGCCATTTATACCATGCTTCAAGAGCCATTCCT 780
Db	
QY	1137 TTTTGGAAACAATGGTGGCCGTTTGTGCATCTGTTTTTTTGTATTTCTCTCAAAATCTTT 1196
Db	
QY	781 TTTTGGAAACAATGGTGGCCGTTTGTGCATCTGTTTTTTTGTATTTCTCTCAAAATCTTT 840
Db	
QY	1197 GTTGGTACAATACTTGGCCGAAATCTGTACAGTCAAGCCCACTTCTTCTGCTGTCAT 1256
Db	
QY	841 GTTGGTACAATACTTGGCCGAAATCTGTACAGTCAAGCCCACTTCTTCTGCTGTCAT 900
Db	
QY	1257 GCTGTGCTGCTCTATACCGGAGAAAAATGTTTCAATGAGGCTCGGGTTATGTTTGC 1316
Db	
QY	901 GCTGTGCTGCTCTATACCGGAGAAAAATGTTTCAATGAGGCTCGGGTTATGTTTGC 960
Db	

QY	1317 CTGGTGGAATTTTACCTTTTGGTTCATCTTATTTGAAATGATTTTCACTTTCAGCTCT 1376
Db	
QY	961 CTGGTGGAATTTTACCTTTTGGTTCATCTTATTTGAAATGATTTTCACTTTCAGCTCT 1020
Db	
QY	1377 TTTCTGGGCATATAAGATCTATTATGCTCTATGGCTTCATGATGCTGGTGGTATTCCTG 1436
Db	
QY	1021 TTTCTGGGCATATAAGATCTATTATGCTCTATGGCTTCATGATGCTGGTGGTATTCCTG 1080
Db	
QY	1437 TGCATTCTGACTCTCTGCTGTGACTATTGTGTGCACATATTTTCTTAAATGCAGAAGAT 1496
Db	
QY	1081 TGCATTCTGACTCTCTGCTGTGACTATTGTGTGCACATATTTTCTTAAATGCAGAAGAT 1140
Db	
QY	1497 TACCGTGGCAATGGACAAGTTTTTCTCTCTGCTGCATCAACTGCAATCTATGTTTACATG 1556
Db	
QY	1141 TACCGTGGCAATGGACAAGTTTTTCTCTCTGCTGCATCAACTGCAATCTATGTTTACATG 1200
Db	
QY	1557 TATTCCTTTTACTTACTATTTTTCACAAACAAAGATGATGGCTTATTTCAACATCATTTT 1616
Db	
QY	1201 TATTCCTTTTACTTACTATTTTTCACAAACAAAGATGATGGCTTATTTCAACATCATTTT 1260
Db	
QY	1617 TACTTTGGATATATGCGGTATTTAGCACAGCCTTGGGGATATGTTGTCGAGCGATT 1673
Db	
QY	1261 TACTTTGGATATATGCGGTATTTAGCACAGCCTTGGGGATATGTTGTCGAGCGATT 1317
Db	
RESULT 9	
AAH13994	
ID	AAH13994 standard; cDNA; 2311 BP.
XX	AAH13994;
AC	XX
XX	XX
DT	26-JUN-2001 (first entry)
XX	XX
DE	Human cDNA sequence SEQ ID NO:11070.
XX	XX
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX	Homo sapiens.
OS	XX
XX	XX
PN	EP1074617-A2.
XX	XX
PD	07-FEB-2001.
XX	XX
PF	28-JUL-2000; 2000EP-0116126.
XX	XX
PR	29-JUL-1999; 99JP-0248036.
PR	27-AUG-1999; 99JP-0300253.
PR	11-JAN-2000; 2000JP-0118776.
PR	02-MAY-2000; 2000JP-0183767.
PR	09-JUN-2000; 2000JP-0241899.
XX	XX
PA	(HELI-) HELIX RES INST.
XX	XX
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX	WPI; 2001-318749/34.
DR	XX
XX	Primer sets for synthesizing polynucleotides, particularly the 5602
PT	full-length cDNAs defined in the specification, and for the detection
PT	and/or diagnosis of the abnormality of the proteins encoded by the
PT	full-length cDNAs -
XX	XX
PS	Claim 8; SEQ ID 11070; 2537pp + CD ROM; English.
XX	XX
CC	The present invention describes primer sets for synthesizing 5602
CC	full-length cDNAs defined in the specification. Where a primer set
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC	to the complementary strand of a polynucleotide which comprises one of
CC	the 5602 nucleotide sequences defined in the specification, where the
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC	of an oligonucleotide comprising a sequence complementary to the
CC	complementary strand of a polynucleotide which comprises a 5'-end



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CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 2299 BP; 649 A; 380 C; 457 G; 813 T; 0 other;

Query Match          60.6%; Score 1090.4; DB 22; Length 2299;
Best Local Similarity 99.9%; Pred. No. 1.1e-272;
Matches 1091; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 709 GAAAGATTATGCTCGGTACAGTAAGAGGAAGAAATGGATGATATGATAGAGACCTAG 768
DB 1 GAAAGATTATGCTCGGTACAGTAAGAGGAAGAAATGGATGATATGATAGAGACCTAG 60

QY 769 GAGATGAATATGGATGGAACAGGTGATGAGATGATTTAGACCATCAAGTCACCCAC 828
DB 61 GAGATGAATATGGATGGAACAGGTGATGAGATGATTTAGACCATCAAGTCACCCAC 120

QY 829 TGATATTTTCTCTCTGATTTGGTTCGGATGTCAGATATTTGCTGTCTCTCATCGTTA 888
DB 121 TGATATTTTCTCTCTGATTTGGTTCGGATGTCAGATATTTGCTGTCTCTCATCGTTA 180

QY 889 TTATTTGTCGAATCATAGAAGATTATATATCTGAGAGGGATCAATGCTCAGTACAGCCA 948
DB 181 TTATTTGTCGAATCATAGAAGATTATATATCTGAGAGGGATCAATGCTCAGTACAGCCA 240

QY 949 TATTTGCTATGCTGCTACGCTCCAGTGAATGGTTATTTGGAGGAAGTCTGTATGCTA 1008
DB 241 TATTTGCTATGCTGCTACGCTCCAGTGAATGGTTATTTGGAGGAAGTCTGTATGCTA 300

QY 1009 GACAAGGAGGAAGAGATGATGAAGAGATGTTATTTGGGCATTCCTTATCCCAGCTA 1068
DB 301 GACAAGGAGGAAGAGATGATGAAGAGATGTTATTTGGGCATTCCTTATCCCAGCTA 360

QY 1069 TGTGTGTGGCACTGCCCTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAG 1128
DB 361 TGTGTGTGGCACTGCCCTCTTCATCAATTTTCATAGCCATTTATTACCATGCTTCAAGAG 420

QY 1129 CCATTCCTTTTGGAAACAATGGTGGCCGTTGTTGCAFCCTGTTTTTTGTTATTTCTCCTC 1188
DB 421 CCATTCCTTTTGGAAACAATGGTGGCCGTTGTTGCAFCCTGTTTTTTGTTATTTCTCCTC 480

QY 1189 TAAATCTTGTGTGTCACATCTTGGCGGAATCTGTGAGTCAGCCCAACTTTCCTTGTCT 1248
DB 481 TAAATCTTGTGTGTCACATCTTGGCGGAATCTGTGAGTCAGCCCAACTTTCCTTGTCT 540

QY 1249 GTGTCAATGCTGTGCCCTGCTTATACCGGAGAAAAATGGTTCATGAGCCCTGCGGTTA 1308
DB 541 GTGTCAATGCTGTGCCCTGCTTATACCGGAGAAAAATGGTTCATGAGCCCTGCGGTTA 600

QY 1309 TTGTTGCCCTGGGTGGGAATTTTACCTTTTGGTTCAATCTTTATTTGAATGTATTTTCATCT 1368
DB 601 TTGTTGCCCTGGGTGGGAATTTTACCTTTTGGTTCAATCTTTATTTGAATGTATTTTCATCT 660

QY 1369 TCAGGCTTTCTGGGCATATAAGATCTATTATGCTATGCTTCATGCTCATGCTGGTCTG 1428
DB 661 TCAGGCTTTCTGGGCATATAAGATCTATTATGCTATGCTTCATGCTCATGCTGGTCTG 720

QY 1429 TTATCTCTGTGCATGTGACTGTCTGTGACTATTGTGTGCACATATTTTCTACTAAATG 1488
DB 721 TTATCTCTGTGCATGTGACTGTCTGTGACTATTGTGTGCACATATTTTCTACTAAATG 780

QY 1489 CAGAAGATTACCGGTGGCAATGAGCAAGTTTCTCTCTGCTGTCATCAACTGCAATCTATG 1548
DB 781 CAGAAGATTACAGGTGGCAATGAGCAAGTTTCTCTCTGCTGTCATCAACTGCAATCTATG 840

QY 1549 TTTACATGTAATCTCTTTTACTACTATTTTTCAAAACAAGATGTATGGCTTATTTCAA 1608
DB 841 TTTACATGTAATCTCTTTTACTACTATTTTTCAAAACAAGATGTATGGCTTATTTCAA 900

QY 1609 CATCATTTTACTTTGGATATATGGCGGTATTTAGCACAGCCTTTGGGGATAATGTGGGAG 1668
DB 901 CATCATTTTACTTTGGATATATGGCGGTATTTAGCACAGCCTTTGGGGATAATGTGGGAG 960

QY 1669 CGATTGGTTACATGGGAACAAGTGCCTTTGTGCCGAAAAATCTATACTAATGTGAAAAATTG 1728
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DB 961 CGATTGGTTACATGGGAACAAGTGCCTTTGTGCCAAAAATCTATACTAATGTAATAATTG 1020
QY 1729 ACTAGACACCAACAACCTGGNACTTTGGATCAATTTCTTTTTCATAGGGTGGAACT 1788
DB 1021 ACTAGACACCAACAACCTGGNACTTTGGATCAATTTCTTTTTCATAGGGTGGAACT 1080
QY 1789 TGCACACGCAAAA 1800
DB 1081 TGCACACGCAAAA 1092

RESULT 11
AAV28121
ID AAV28121 standard; DNA; 965 BP.
XX AAV28121:
XX
XX 25-SEP-1998 (first entry)
DE Non-adrenergic SM-binding protein 900 bp probe.
XX
XX Non-adrenergic SM binding protein; human; muscle; receptor; ss; probe;
KW Iodocyanopindolol.
XX
XX Homo sapiens.
XX
XX EP848059-A1.
XX
XX 17-JUN-1998.
XX
XX 12-DEC-1996; 96EP-0402719.
XX
XX 12-DEC-1996; 96EP-0402719.
XX
XX (VETI-) VETIGEN.
XX
XX Lenzen G, Morooka S, Strosberg AB, Sugawara T;
XX WPI; 1998-314474/28.
XX
XX New iodocyanopindolol receptor polypeptide - and corresponding DNA,
XX antibodies, etc.
XX
XX Claim 5; Page 23-24; 56pp; English.
XX
XX The probes AAV28121-V28122 were used in the isolation of non-adrenergic
XX receptors from human skeletal muscle. This includes the non-adrenergic
XX SM binding protein which is a member of a novel receptor class which
XX have a receptor activity other than that of beta3-adrenergic receptors.
XX The protein comprises sites which, when exposed on the cell surface, are
XX capable of binding iodocyanopindolol (ICYP) under blockade of alpha
XX beta 1, beta 2 and beta 3 adrenergic receptors and serotonin 5-HT1A and
XX 5-HT1B receptors. The binding is saturable and reversible by
XX displacement with the stereoselective beta-adrenergic receptor agonist
XX SM-11044 but not isoproterenol, epinephrine, norepinephrine, serotonin,
XX dopamine or BRL-37344.
XX
XX Sequence 965 BP; 246 A; 163 C; 214 G; 342 T; 0 other;

Query Match          53.5%; Score 963.4; DB 19; Length 965;
Best Local Similarity 99.9%; Pred. No. 7e-240;
Matches 964; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 531 CAGATGTCATATTTCAGTAAATGAAAACTCAGATGTGAAATTTGAAGATCGATTGAC 590
DB 1 CAGATGTCATATTTCAGTAAATGAAAACTCAGATGTGAAATTTGAAGATCGATTGAC 60
QY 591 AAATATCTTCATCGCTCTTTTTCACATCGGATTCATTTGGTTTCAATTTCAACTCC 650
DB 61 AAATATCTTCATCGCTCTTTTTCACATCGGATTCATTTGGTTTCAATTTCAACTCC 120
QY 651 TTCATGATGTGATCTTCTTTGGTGGGCTTAGTTTCAATGATTTTAAATGAGAACAATTAAGA 710
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Db	241	TCAGTACAGCCATATTGTCTATGCTGCTACGTCCTCAGTGAATGGTTATTGTGGAGAA	300
Qy	997	GTCCTGATGCTAGACAAGGAGGAGATGGATAAAGCAGATGTTTATTGGGGCATTTCC	1056
Db	301	GTCCTGATGCTAGACAAGGAGGAGATGGATAAAGCAGATGTTTATTGGGGCATTTCC	360
Qy	1057	TTATCCAGCTATGGTGCTGGGCACATGCTTCTTCATCAATTTTCATAGCCATTTATTACC	1116
Db	361	TTATCCAGCTATGGTGCTGGGCACATGCTTCTTCATCAATTTTCATAGCCATTTATTACC	420
Qy	1117	ATGCTTCAAGAGCCATTCCTTTTGGGAACAATGGTGCCCGTTTGTTCATCTGTTTTTTG	1176
Db	421	ATGCTTCAAGAGCCATTCCTTTTGGGAACAATGGTGCCCGTTTGTTCATCTGTTTTTTG	480
Qy	1177	TTATTTCTTCCTCTAAATCTTTGTTGGTACAAATCTTGGCCGAAATCTGTCAGGTCAGCCCA	1236
Db	481	NTATTTCTTCCTCTAAATCTTTGTTGGTACAAATCTTGGCCGAAATCTGTCAGGTCAGCCCA	540
Qy	1237	ACTTTCCCTTGGCTGTGCAATGCTGTGCCTCGTCTATACCGGAGAAAAATGGTTTCATGG	1296
Db	541	ACTTTCCCTTGGCTGTGCAATGCTGTGCCTCGTCTATACCGGAGAAAAATGGTTTCATGG	600
Qy	1297	AGCCTGGCGTTATTGTTTGGCTGGGTGGAAATTTTACCTTTGGTTCATCTTTATTGAAA	1356
Db	601	AGCCTGGCGTTATTGTTTGGCTGGGTGGAAATTTTACCTTTGGTTCATCTTTATTGAAA	660
Qy	1357	TGTAATTTCACTTTCACGCTCTTTCTGGGCAAT - AAGATCTATTATGTCAT - GGCTTCAT	1414
Db	661	TGTAATTTCACTTTCACGCTCTTTCTGGGCAAT - AAGATCTATTATGTCAT - GGCTTCAT	720
Qy	1415	GATGCTGGTCTGGTTATCCTGTGCATTTGACTGTCTGTGACTATTGTGTGCACATA	1474
Db	721	GATGCTGGTCTGGTTATCCTGTGCATTTGACTGTCTGTGACTATTGTGTGCACATA	780
Qy	1475	TT 1476	
Db	781	TT 782	
RESULT 13			
ABL90852			
ID	ABL90852 standard; cDNA; 1070 BP.		
XX	ABL90852;		
XX	24-MAY-2002 (first entry)		
DT	Human polynucleotide SEQ ID NO 1414.		
DE	Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;		
DE	antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;		
KW	vulnerable; anticonvulsant; antibacterial; antifungal; antiparasitic;		
KW	cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;		
KW	neurological disease; infection; human; secreted protein; gene; ss.		
OS	Homo sapiens.		
XX	WO200190304-A2.		
PN	29-NOV-2001.		
XX	18-MAY-2001; 2001WO-US16450.		
PF	19-MAY-2000; 2000US-205515P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
PR	Birse CE, Rosen CA;		
PA	WPI; 2002-122018/16.		
PA	P-PSDB; ABB90443.		
XX			
XX			

Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders -

Claim 4; SEQ ID NO 1414; 2081pp + Sequence Listing; English.

The invention relates to novel genes (AB189449-AB190853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

Sequence 1070 BP; 262 A; 206 C; 227 G; 363 T; 12 other;

Query Match 39.8%; Score 716.4; DB 24; Length 1070;  
Best Local Similarity 92.6%; Pred. No. 9.9e-176;  
Matches 803; Conservative 0; Mismatches 11; Indels 53; Gaps

Qy 987 TTTCGGAGGAATCTGTATGCTAGACAAGGAGGAGATGCATAAAGCAGATGTTTATT 1048  
||||| |||||  
Db 20 TTTCGGAGGCTCTCTNTATGANACACAGGAGGAGGACATGCATTAACGACATGTTTATT 79

Qy 1047 GGGGCATTCCTTATCCAGACTATGGTGTTGGCACGCCCTCTTCATCAAAATTCATAGCC 1106  
||||| |||||  
Db 80 GGGGCATTCCTTATCCAGACTATGGTGTTGGCACGCCCTCTTCATCAAAATTCATAGCC 139

Qy 1107 ATTTATTACCATGCTTCAAGAGCCATTCCTTTTGGAACAAATGGTGGCGGTTTGTTCATC 1166  
||||| |||||  
Db 140 ATTTATTACCATGCTTCAAGAGCCATTCCTTTTGGAACAAATGGTGGCGGTTTGTTCATC 199

Qy 1167 TGTTTTTTTTGTTATTCCTCTCTAAATCTTGTTGGTACAAATACTTTGGCGGAATCTGTCA 1226  
|||||  
Db 200 TGTTTTTTTTGTTATTCCTCTCTAAATCTTGTTGGTACAAATACTTTGGCGGAATCTGTCA 259

Qy 1227 GGTCAGCCCCAACTTCCTTGCTGCTGCAATGCTGTGCCCTGCCTCATACCGGAGAAAAA 1286  
|||||  
Db 260 GGTCAAGCCCAACTTCCTTGCTGCTGCAATGCTGTGCCCTGCCTCATACCGGAGAAAAA 319

Qy 1287 TGGTTTCATGAGCGCTGGGTTATTGTTTGCCTGGGTGGAAATTTTACCCTTTGGTTCATC 1346  
|||||  
Db 320 TGGTTTCATGAGCGCTGGGTTATTGTTTGCCTGGGTGGAAATTTTACCCTTTGGTTCATC 379

Qy 1347 TTTATTCAAATGTATTTCATCTTCACGTCCTTCTGGGCATATAAAGATCTATTATGTCAT 1406  
|||||  
Db 380 TTTATTCAAATGTATTTCATCTTCACGTCCTTCTGGGCATATAAAGATCTATTATGTCAT 439

Qy 1407 GGCATTATGATGCTGGTGGTATTATTCCTGTGCATTTGTGACTGTCTGTGACTATTGTG 1466  
|||||  
Db 440 GGCATTATGATGCTGGTGGTATTATTCCTGTGCATTTGTGACTGTCTGTGACTATTGTG 499

Qy 1467 TGCACATATTTTCTACTAAATGACAAA --GATTAACGGT----- 1503  
||||| |||||  
Db 500 TGCACATATTTTCTACTAAATGACNAAGNATTAACGGTGTGCCCATTCATTCAAAGNAG 559  
|||||  
Qy 1504 -----GGCAATGGACAAGTTTTCTCTCGCTGCATC 1534  
|||||  
Db 560 ATTTATTCCTTCTCCCGCTCCCGCCACAGGCAATGGACAAGTTTTCTCTCGCTGCATC 619

Qy 1535 AACTGCAATCTATGTTTACATGATGTTATTCCTTTTACTACTATTTTTTTTCAAAACAAGATGTA 1594

|||||  
Db 620 AACTGCAATCTATGTTACATCTATTCCTTTTACTACTATTTTTCACAAACAAAGATGTA 679  
QY 1595 TGGCTTATTTCAACATCATTTTACTTTGGATATATGCGGTATTTAGCACAGCCTT-GG 1653  
Db 680 TGGCTTATTTCAACATCATTTTACTTTGGATATATGCGGTATTTAGTACAGCCTTGGG 739  
QY 1654 GGATAATGTGTGGAGCGATTGGTTACATGGGAACAGTGCCTTTGTGCGAAAAATCTATA 1713  
Db 740 GGATAATGTGTGGAGCGATTGGTTACATGGGAACAGTGCCTTTGTGCGAAAAATCTATA 799  
QY 1714 CTAATGTGAAAAATGACTAGAGACCCCAAGAAACCTGGAACCTTTGGATCAATTTCTTTT 1773  
Db 800 CTAATGTGAAAAATGACTAGAGACCCCAAGAAACCTGGAACCTTTGGATCAATTTCTTTT 859  
QY 1774 CATAGGGTGGAACTTGCACAGCAAAA 1800  
Db 860 CATAGGGTGGAACTTGCACAGCAAAA 886  
  
RESULT 14  
AAK92142  
ID AAK92142 standard; cDNA: 756 BP.  
XX AC  
XX AAK92142;  
XX DT  
XX 06-NOV-2001 (first entry)  
XX DE Human cDNA 5'-end sequence, SEQ ID NO: 602.  
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX OS Homo sapiens.  
XX PN EP1130094-A2.  
XX PD 05-SEP-2001.  
XX PF 07-JUL-2000; 2000EP-0114089.  
XX PR 08-JUL-1999; 99JP-0194486.  
XX PR 11-JAN-2000; 2000JP-0118774.  
XX PR 02-MAY-2000; 2000JP-0183765.  
XX PA (HELI-) HELIX RES INST.  
XX PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
XX PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX WPI; 2001-524255/58.  
XX  
XX 830 Primers useful for synthesizing full length cDNA clones and their  
XX use in genetic manipulation -  
XX  
XX Claim 2; SEQ ID NO 602; 1380pp + sequence listing; English.  
XX  
XX The invention relates to primers for synthesising full length cDNA  
XX clones. 830 cDNA molecules encoding a human protein have been  
XX isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
XX molecules have been determined. Primers for synthesising the full length  
XX cDNA are useful for clarifying the function of the protein encoded by  
XX the cDNA. The full length clones were obtained by construction of full  
XX length enriched cDNA libraries that were synthesised by the oligo-capping  
XX method. The primers enable the production of the full length cDNA easily  
XX without any special methods. The present sequence is the nucleotide  
XX sequence of the 5'-end of a cDNA provided in the invention.  
XX Note: The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in CD-ROM format directly from EPO.  
XX  
XX Sequence 756 BP; 183 A; 135 C; 182 G; 251 T; 5 other;  
  
Query Match 38.7%; Score 696.6; DB 22; Length 756;  
Best Local Similarity 99.3%; Pred. No. 1.2e-170;

Matches 710; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
QY 709 GAAAGATTATGCTCGGTACAGTAAAGAGGAGAAATGGATGATATGGATAGAGACCTAG 768  
Db 1 GAAAGATTATGCTCGGTACAGTAAAGAGGAGAAATGGATGATATGGATAGAGACCTAG 60  
QY 769 GAGATGAATATGGATGGAACACAGGTGCATGGAGATGTATTTAGACCATCAAGTACCCAC 828  
Db 61 GAGATGAATATGGATGGAACACAGGTGCATGGAGATGTATTTAGACCATCAAGTACCCAC 120  
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AAK93404  
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XX AC  
XX AAK93404;  
XX DT 06-NOV-2001 (first entry)  
XX DE Human cDNA clone representative sequence, SEQ ID NO: 1864.  
XX KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.  
XX OS Homo sapiens.  
XX PN EP1130094-A2.  
XX PD 05-SEP-2001.  
XX PF 07-JUL-2000; 2000EP-0114089.  
XX PR 08-JUL-1999; 99JP-0194486.  
XX PR 11-JAN-2000; 2000JP-0118774.

02-MAY-2000; 2000JP-0183765.

(HELI-) HELIX RES INST.

Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
WPI; 2001-524255/58.

830 Primers useful for synthesizing full length cDNA clones and their  
use in genetic manipulation -

Example 11; SEQ ID NO 1864; 1380pp + sequence listing; English.

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO.

Sequence 756 BP; 183 A; 135 C; 182 G; 251 T; 5 other;

Query Match 38.7%; Score 696.6; DB 22; Length 756;  
Best Local Similarity 99.3%; Pred. No. 1.2e-170;  
Matches 710; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 769 GAGATGAATATGATGGAACAGGTGCATGGAGATGATTTAGACCATCAAGTCACCCAC 828

Db 61 GAGATCAATATGGATGGAACAGGTGCATGGAGATGATTTAGACCATCAAGTCACCCAC 120

QY 829 TGATATTTTCCCTCTCGATTGGTTCGGATGTCAGATATTTGCTGTCTCTCATCGTTA 888

Db 121 TGATATTTTCCCTCTCGATTGGTTCGGATGTCAGATATTTGCTGTCTCTCATCGTTA 180

QY 889 TTATTCGTCGAATGATAGAAATTTATATACTGAGAGGGATCAATGCTCAGTACAGCCA 948

Db 181 TTATTCGTCGAATGATAGAAATTTATATACTGAGAGGGATCAATGCTCAGTACAGCCA 240

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Job time : 404 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2003, 07:18:30 ; Search time 4565 Seconds  
(without alignments)  
11475.367 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
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Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: gb\_pat : \*  
7: gb\_ph : \*  
8: gb\_pl : \*  
9: gb\_pr : \*  
10: gb\_ro : \*  
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37: em\_htg\_vrt : \*  
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39: em\_htgo\_hum : \*  
40: em\_htgo\_mus : \*  
41: em\_htgo\_other : \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1798.4	99.9	3592	9	AF269150	AF269150 Homo sapi
4	1709	94.9	3389	9	AF160213	AF160213 Homo sapi
5	1708.4	94.9	2459	9	AK027788	AK027788 Homo sapi
6	1632.4	90.7	2870	9	BC020959	BC020959 Homo sapi
7	1551	86.2	3143	10	AF269151	AF269151 Mus muscu
8	1450.6	80.6	2973	9	AK000756	AK000756 Homo sapi
9	1386.2	77.0	2848	10	BC004799	BC004799 Mus muscu
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17	577.8	32.1	2062	8	AY054666	AY054666 Arabidops
18	577.8	32.1	2094	8	AF446365	AF446365 Arabidops
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21	563.6	31.3	163115	3	AC010661	AC010661 Drosophil
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ALIGNMENTS

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VERSION	A91337.1	GI:6740338				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

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Q	y	1681	TGGGAACAAGTGCCTTTGTCGGAAAAATCTATACTAATGTGAAATTTGACTTAGAGACCCA	1740
D	b	1935	TGGGAACAAGTGCCTTTGTCGGAAAAATCTATACTAATGTGAAATTTGACTTAGAGACCCA	1994
Q	y	1741	AGAAACCTGGAACCTTTGGATCAATTTCTTTTTCATAGGGGTGGAACCTTGCCACAGCAAA	1800
D	b	1995	AGAAACCTGGAACCTTTGGATCAATTTCTTTTTCATAGGGGTGGAACCTTGCCACAGCAAA	2054
RESULT 4				
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LOCUS	AF160213	3389 bp	mRNA	linear PRI 02-MAY-2000
DEFINITION	Homo sapiens endomembrane protein emp70 precursor isolog mRNA, complete cds.			
ACCESSION	AF160213			
VERSION	AF160213.1 GI:7677067			
KEYWORDS	Homo sapiens.			
SOURCE	Homo sapiens.			
ORGANISM	Homo sapiens.			

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 3389)  
REFERENCE  
AUTHORS  
Gu,Y., Peng,Y., Li,Y., Fu,S., Gu,J., Gu,W., Jiang,C., Yu,Y., Han,Z., Wang,Y., Chen,Z. and Fu,G.  
A novel gene expressed in human adrenal gland  
Unpublished  
2 (bases 1 to 3389)  
Peng,Y., Gu,Y., Li,Y., Fu,S., Gu,J., Zhang,L., Jiang,C., Yu,Y., Han,Z., Wang,Y., Chen,Z. and Fu,G.  
Direct Submission  
TITLE  
JOURNAL  
Submitted (18-JUN-1999) Chinese National Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China  
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DB 54 CCGCCGCGCTGTGCTGCTGCTGCTGCTGCTGCCCGCGGACCCCGGGCGGACGACGACCAAC 113  
QY 61 ACAGGTATCAAGATAAAGAGGAAGTTGTCTTATGGATGAATACTGTGTGGCCCTACCATA 120  
DB 114 ACAGGTATCAAGATAAAGAGGAAGTTGTCTTATGGATGAATACTGTGTGGCCCTACCATA 173  
QY 121 ATCGTCAAGAACATATAAGTACTTTTCACTTCCATTTCTGTGGGGTCAAAAAAAGTA 180  
DB 174 ATCGTCAAGAACATATAAGTACTTTTCACTTCCATTTCTGTGGGGTCAAAAAAAGTA 233  
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DB 234 TCAGTCAATTACCATGAACTCTGGGAGAAGCACTTCAAGGGGTGAATTGGAATTTAGTG 293  
QY 241 GTCTGGATTTAAATTTAAAGATGATGTGATGCCAGCCACTTACTGTGAAATTTAGTTAG 300  
DB 294 GTCTGGATTTAAATTTAAAGATGATGTGATGCCAGCCACTTACTGTGAAATTTAGTTAG 353  
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DB 414 ACATAGATGATTTACCAATATGGGTATGTTGGTGAGGCTGATGAAATGGAGAGATT 473  
QY 421 ACTATCTTTGGACCTATAAAAAACTTCAAAATAGSTTTTAAATGAAATCGAATTTGTTGATG 480



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QY	151	TTCCATTCTCTGTGGGTCACAAAAAGATATCAGTCAATTACCATGAACCTCTGGGAGAAG	210
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QY	211	CACCTCAAGGGTGAATTTAGTGGTCTGGATATAAATTTAAAGATGATGTGA	270
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QY	271	TGCCAGCCACTTACTGTGAAATTCATTTAGATAAGAAAGAGAGATGCGATTTGTATATG	330
DB	181	TGCCAGCCACTTACTGTGAAATTCATTTAGATAAGAAAGAGAGATGCGATTTGTATATG	240
QY	331	CCATAAAAAATCAATTACTGGTACCAGATGTACATAGATGATTTACCAATATGGGGTATTG	390
DB	241	CCATAAAAAATCAATTACTGGTACCAGATGTACATAGATGATTTACCAATATGGGGTATTG	300
QY	391	TTGGTGAGGCTGATGAAANTGGAGAACTTACTATCTTTGGACCTATAAAAACTTGAAA	450
DB	301	TTGGTGAGGCTGATGAAANTGGAGAACTTACTATCTTTGGACCTATAAAAACTTGAAA	360
QY	451	TAGGTTTTAATGGAATCGAATCTTCATGTTAATCTAATCTAGTGAAGGAAAGGTGAAC	510
DB	361	TAGGTTTTAATGGAATCGAATCTTCATGTTAATCTAATCTAGTGAAGGAAAGGTGAAC	420
QY	511	TGGTTCCAAATACTAAATCCAGATGTCATATTCAGTAAAAATGAAAAAGTCAGATGTGA	570
DB	421	TGGTTCCAAATACTAAATCCAGATGTCATATTCAGTAAAAATGAAAAAGTCAGATGTGA	480
QY	571	AATTTGAAGATCGATTTGACAAATATCTTGATCGGTCCTTTTTCACATCGGATTCATT	630
DB	481	AATTTGAAGATCGATTTGACAAATATCTTGATCGGTCCTTTTTCACATCGGATTCATT	540
QY	631	GGTTTTCAATTTTCAACTCTTCATGATGTTGATCTTCTGGTGGCTTAGTTTCAATGA	690
DB	541	GGTTTTCAATTTTCAACTCTTCATGATGTTGATCTTCTGGTGGCTTAGTTTCAATGA	600
QY	691	TTTTTAATGAGAACAATTAAGAAAAGATTATGTCGCGTACAGTAAAGAGAGAAAATGGATG	750
DB	601	TTTTTAATGAGAACAATTAAGAAAAGATTATGTCGCGTACAGTAAAGAGAGAAAATGGATG	660
QY	751	ATATGGATAGAGACCTAGGAGATGAATATGATGGAACACAGGTCATGGAGATGATTTTA	810
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DB	721	GACCATCAAGTCACCCACTGATATTTTCTCTGATTTGGTCTCGGATGTGAGATATTTG	780
QY	871	CTGTGCTCTCATGCTTATTATTGTTGCAATGATAGAAAGATTTATATCATGAGGGGAT	930
DB	781	CTGTGCTCTCATGCTTATTATTGTTGCAATGATAGAAAGATTTATATCATGAGGGGAT	840
QY	931	CAATGCTCAGTACAGCCATATTTGCTGATGCTGCTACGTCCTCCAGTGAATGGTTATTTG	990
DB	841	CAATGCTCAGTACAGCCATATTTGCTGATGCTGCTACGTCCTCCAGTGAATGGTTATTTG	900

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QY	1051	CATTCCCTATCCAGCTATGCTGTGGGCTGCTTCTTTCATCAATTTTCATAGCCATTT	1110
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QY	1171	TTTTTTGTTATTTCTTCCCTCTAAATCTTGTGTACAATACTTGGCCGAAAATCTGTACAGTC	1230
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QY	1231	AGCCAACTTTCCCTTGTCTCAATGCTGTCCCTCGCTCTATACCCGAGAAAATGGT	1290
DB	1141	AGCCAACTTTCCCTTGTCTCAATGCTGTCCCTCGCTCTATACCCGAGAAAATGGT	1200
QY	1291	TCATGGAGCCTGGGTTTATTTGTTTGCCTGGTGGTGAATTTTACCTTTTGGTTCAATCTTTA	1350
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QY	1351	TTGAAATGTTATTCATCTTTCACGCTTCTTTCGGGCATATAAGATCTATATGCTATGGCT	1410
DB	1261	TTGAAATGTTATTCATCTTTCACGCTTCTTTCGGGCATATAAGATCTATATGCTATGGCT	1320
QY	1411	TCATGATGCTGGTGGTGTATCTGTGCAATGTGACTGTGTGTGACTATTTGTGTGCA	1470
DB	1321	TCATGATGCTGGTGGTGTATCTGTGCAATGTGACTGTGTGTGACTATTTGTGTGCA	1380
QY	1471	CATATTTTCTACTAAATGCGAGAAGATTACCGTGGCAATGGACAAGTTTCTCTCTGCTG	1530
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DB	1501	TGATGCTTATTTTCAACATCATTTTACTTTTGGATATATGGGGTATTTAGCACAGCCT	1560
QY	1651	TGGGTAATGCTGTGGAGCGATTGGTTTACATGGGAAACAGTGCCTTTTGTCCGAAAATCT	1710
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DB	1681	TTTCATAGGGTGGAACTTGCACAGCAAAA	1710

RESULT 6  
BC020959  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

BC020959  
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BC020959  
BC020959.1 GI:18088072  
MGC.  
Homo sapiens.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 2870)  
Strausberg, R.  
Direct Submission  
Submitted (03-JAN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgabp@remail.nih.gov](mailto:cgabp@remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mdpaxil@stanford.edu](mailto:mdpaxil@stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 20 Row: 1 Column: 13.

FEATURES

source

Location/Qualifiers

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BASE COUNT 866 a 447 c 568 g 989 t

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RESULT 7
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DEFINITION
cds.
ACCESSION AF269151
VERSION AF269151.1 GI:9755052
KEYWORDS
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3143)
Warner, S.J. and Lomax, M.I.
Evolution of the TM9 Super Family of Membrane Spanning Proteins
Unpublished
2 (bases 1 to 3143)
Warner, S.J. and Lomax, M.I.
Direct Submission
Submitted (10-MAY-2000) Kresge Hearing Research Institute,
University of Michigan, 9301E MSRB III, 1150 West Medical Center
Drive, Ann Arbor, MI 48109-0648, USA
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QY	944	AGCCATATTTCTCTATGCTGTAGCTCTCCAGTGAATGGTTATTTTGGAGGAAGTCTGTA	1003
Db	601	AGCCATATTTCTCTATGCTGTAGCTCTCCAGTGAATGGTTATTTTGGAGGAAGTCTGTA	660
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RESULT	9		
LOCUS	BC004799	2848 bp	linear
DEFINITION	Mus musculus, clone MGC:8136	IMAGE:3589474	mrna
ACCESSION	BC004799		
VERSION	BC004799.1	GI:13435914	
KEYWORDS	MGC.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
			ROD 07-AUG-2002
			complete cds.

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RESULT 10
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LOCUS A78983 1317 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 2 from Patent EP0848059.
ACCESSION A78983
VERSION A78983.1 GI:6092106
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1317)
AUTHORS Lenzen,G. and Strosberg,A.D.
TITLE MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS
JOURNAL Patent: EP 0848059-A 2 17-JUN-1998;
VETIGEN (FR)
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Query Match 73.2%; Score 1317; DB 6; Length 1317;
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Matches 1317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 597 CTTGATCCGCTCTTTTTCACATCGGATTCATTGGTGTTCATTTTCAATTTTCAACTCCTTCATG 656
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RESULT 11

A91326  
LOCUS 1317 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 2 from Patent WO9826065.  
ACCESSION A91326  
VERSION A91326.1 GI:6740329

KEYWORDS unidentified.  
SOURCE unidentified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 1317)  
AUTHORS Lenzen,G. and Strosberg,A.D.  
TITLE MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS  
JOURNAL Patent: WO 9826065-A 2 18-JUN-1998;  
VETIGEN (FR); LENZEN GERLINDE (FR)  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 355 a 211 c 288 g 463 t  
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Query Match 73.2%; Score 1317; DB 6; Length 1317;  
Best Local Similarity 100.0%; Pred. No. 1.2e-292;  
Matches 1317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 12  
AK027438  
LOCUS  
DEFINITION  
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to ENDOSONAL P24A PROTEIN PRECURSOR.  
AK027438  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
oligo capping; fis (full insert sequence).  
Homo sapiens teratocarcinoma cell line: NT2 cDNA to mRNA,  
clone lib: NT2RM2 clone: NT2RM2000402.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,  
Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,  
Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H.,  
Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K.,  
Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,  
Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,  
Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.  
NEDO human cDNA sequencing project  
Unpublished  
TITLE  
JOURNAL  
2 (bases 1 to 2311)  
REFERENCE  
Isogai, T. and Otsuki, T.  
Direct Submission  
TITLE  
JOURNAL  
Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,  
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
NEDO human cDNA sequencing project supported by Ministry of  
Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
Research Association for Biotechnology; cDNA library construction;  
5'- & 3'-end one pass sequencing and clone selection; Helix  
Research Institute (supported by Japan Key Technology Center etc.)  
and Department of Virology, Institute of Medical Science,  
University of Tokyo.  
LOCATION/Qualifiers

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DEFINITION Sequence 3 from Patent EP0848059.  
ACCESSION A78984  
VERSION A78984.1 GI:6092107  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE  
1 (bases 1 to 965)  
Lenzen, G. and Strosberg, A. D.  
TITLE MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS  
JOURNAL Patent: EP 0848059-A 3 17-JUN-1998;  
VETIGEN (FR)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 99.9%; Pred. No. 3.1e-211;

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A91327

LOCUS A91327

DEFINITION Sequence 3 from Patent WO9826065.

ACCESSION A91327

VERSION A91327.1 GI:6740330

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 965)

Lenzen, G. and Strosberg, A. D.

TITLE MAMMALIAN ICYP (IODOCYANOPINDOLOL) RECEPTOR AND ITS APPLICATIONS

JOURNAL Patent: WO 9826065-A 3 18-JUN-1998;

VETIGEN (FR); LENZEN GERLINDE (FR)

FEATURES

source Location/Qualifiers

I. .965

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/db\_xref="taxon:32644"

BASE COUNT 246 a 163 c 214 g 342 t



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GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: January 20, 2003, 14:15:05 ; Search time 50 seconds  
(without alignments)  
1107.469 Million cell updates/sec

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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1668	54.0	589	2 D86243	hypothetical prote
2	1146.5	37.1	592	2 D84431	probable endosomal
3	918	29.7	656	2 T28058	hypothetical prote
4	898	29.1	659	2 D84633	probable multisp
5	854	27.6	637	2 H96592	probable multisp
6	847.5	27.4	655	2 T32472	hypothetical prote
7	843	27.3	639	2 T50793	hypothetical prote
8	694	22.5	667	2 S64915	EMP70 protein prec
9	688	22.3	629	2 T39285	probable transmem
10	667.5	21.6	672	2 S2673	probable membrane
11	650	21.0	527	2 H85135	hypothetical prote
12	447	14.5	260	2 H86280	protein F10B6.2 [i
13	438	14.2	706	2 S0616	hypothetical prote
14	121	3.9	605	2 H95240	conserved hypothet
15	121	3.9	605	2 A9705	hypothetical prote
16	119	3.9	578	1 F64578	oligoendopeptidase
17	117.5	3.8	417	2 F97789	ampg protein [limp
18	117.5	3.8	820	2 A40204	Na+/H+-exchanging
19	115	3.7	502	1 I30010	NADH2 dehydrogenas
20	115	3.7	528	2 S05063	hypothetical prote
21	115	3.7	578	2 B71934	oligopeptidase - H
22	114	3.7	478	2 T11318	NADH2 dehydrogenas
23	113	3.6	570	2 T06624	NADH2 dehydrogenas
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25	112	3.6	792	2 G84830	probable potassium
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27	110.5	3.6	2848	2 T32550	hypothetical prote
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29	110	3.6	818	2 A48858	Na+/H+-exchanging

RESULT 1

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C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: D86243

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
ausen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: D86243

A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-589 <STO>  
A:Cross-references: GB:AE005172; NID:g1931647; PIDN:AAB65482.1; GSPDB:GN00141  
C:Genetics:  
A:Map position: 1  
C:Superfamily: Schizosaccharomyces pombe probable transmembrane protein SPBC1105.08

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ALIGNMENTS

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 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 16-Feb-2001  
 C:Accession: D84431  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayan, L.; Tallon, L.;  
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: AB4420; MUID:20083487; PMID:10617197  
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 A:Status: preliminary  
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 A:Gene: At2g01970  
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 Best Local Similarity 36.9%; Pred. No. 3.3e-81;  
 Matches 214; Conservative 125; Mismatches 214; Indels 27; Gaps 10;  
 Qy 14 RADEHTYQDKKEEVLNMTVGPYHNQETKYFSLPFCVSGSKSIHYHETLGEALQ 73  
 Db 23 RSDASDRYKDGSLVPLANKVGPFPNPFSEYRYFDLPFCI--PGVKDKKEALGEVLNG 80  
 Qy 74 VLEFSGLDIKFKDDVMPATYCEIDLKREKDAFYAIKNNHYQMYIDDLPIWGIVGEA 133  
 Db 81 DRLVSAPYKLNFRDEKDESEVYCKKLSREEVEHFRRAVEKDYFYQMYDDLPIWGIVGEA 140  
 Qy 134 DENGED-----YYLWTKKLBIGNGRIVDVN--LTSSEKVKLVPTNKT--QMSYSVK 183  
 Db 141 DKESKSDPSEFYKLYKHQIFELYNKDRVIEINARMDPHSLVOLTEDEKVEDAEFMYTVK 200  
 Qy 184 WKSDVKFEDRDKYLDPSFFOH--RIHWFSLFNFMVIFVLGVLSMLMRLTKRKYAR 241  
 Db 201 WKETSTSEKMDKYAMSSSLPHHLEIHWFSILNSCVTVLLTGLFATILMRVLKNDPFWK 260  
 Qy 242 YSKEEMDDMDRLDGEDYGWKGVHGDVFRPSHPILFSSLSGSCQIFAVSLIIVAMI 301  
 Db 261 YAQDEAAD-DQ--EETGWKYIHGDVFRFPKNKSLFAASLGSQGLTTLTIFIMLSIV 316  
 Qy 302 EDLYT-ERGSMLSTAIYVAAATSPVNGVFGGSLYARQGRRWIKOMFTGAFILPAMVCGT 360  
 Db 317 GVFPYNRGALFTALVYALTSGIATSSAFYQCLEGNWVRNL---LLTGLFLFCGP 372  
 Qy 361 AF----FINFIAIYHASRAIPFGFMVAVCCICFVILPLNLVGTILGNLSGPNPCRV 416  
 Db 373 LFLTFCFLNTVAIYASATAALPFGIITVILWTLVTSFLLVGLGIAGKNSKAEPQAPVR 432

Qy 417 VNAVPRPIPEKKWMEPAVIVCLGILPGSIFITMYFIPTSFWAYKIYVYVGMMLVLV 476  
 Db 433 TTKYPREIPLPWYRSASVPOMAMAGELPFSAIYIELYIFASVGMGHRITTYISILFIVI 492  
 Qy 477 ILCLVTVCTIVCYFLLNAEDYRWQWTSFSAASTAIYVYVYFYYFRTKMYGLPQTSFY 536  
 Db 493 ILLIVTAFITVATYFQAAEDHEWNRSFCCGGSTGLFIYAYCLYIYYSARSDMSGFMQT 552  
 Qy 537 SFYCYMAVFSTALGIMCGAIGYMGCTSAFVRKIYTNVKID 576  
 Db 553 SFFPGYMACICYGFLMLGTGVFRAALLFVRHIYRSIKCE 592  
 RESULT 3  
 T28058  
 hypothetical protein ZK858.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T28058  
 R:White, S.  
 submitted to the EMBL Data Library, September 1996  
 A:Reference number: Z20462  
 A:Accession: T28058  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-656 <WIL>  
 A:Cross-references: EMBL:Z79759; PIDN:CA802141.1; GSPDB:GN00019; CESP:ZK858.6  
 A:Experimental source: clone ZK858  
 C:Genetics:  
 A:Gene: CESP:ZK858.6  
 A:Map position: 1  
 A:Introns: 1/3; 36/3; 78/3; 165/2; 222/2; 309/1; 377/1; 537/3; 596/1; 623/2  
 C:Superfamily: Schizosaccharomyces pombe probable transmembrane protein SPBC1105.08  
 Query Match 29.7%; Score 918; DB 2; Length 656;  
 Best Local Similarity 33.9%; Pred. No. 2.le-63;  
 Matches 195; Conservative 110; Mismatches 218; Indels 52; Gaps 9;  
 Qy 45 KYFSLPFCVSGSKSIHYHETLGEALQVELEFSGLDIKFKDDVMPATYCEIDLKREK 104  
 Db 91 FEYSVPFCCKPANGDIQYKSNLGEVMEGRDRIVNTPTPYAFHMKNEQCVSVCSNLSKENV 150  
 Qy 105 DAFVYAIKNNHYQMYIDDLPIWGIVGEADENGEDYIYLTWTKKLEIGFNGN----- 155  
 Db 151 ALFERIRQEYSAHLIVDNLPVATVINPA-QSGDVYVYDLYGRLGWIGDNVAKVFLNNHQLF 209  
 Qy 156 -----RIVDVNLTSEKVKLVFN-TK-----IQMSYSVK 183  
 Db 210 VVKYHQHTPGLYRVVGFVRPRPSISATKNDGTCMPDDGKHVELGDSQSVDFSYVA 269  
 Qy 184 WKSDVKFEDRDKYLDPSFFQHRHWFSLFNFMVIFVLGVLSMLMRLTKRKYARYS 243  
 Db 270 FEESDVPWASRDVYLTTKAVD--IHWFSILNSIVVLSLGSFVSVTIVTRVRRDIAQYN 327  
 Qy 244 KEEMDDMDRLDGEDYGWKGVHGDVFRPSHPILFSSLSGSCQIFAVSLIIVAMLED 303  
 Db 328 RDDEED----DLTEETGWKLVHGDVFRPPHOMILVNNVGTGIQLLGNLSAIVVYCAMLGM 383  
 Qy 304 LY-TERGSMSTAIYVAAATSPVNGYFGGSLYARQGRRWIKOMFAGIFLIPAMVCGTAF 362  
 Db 384 LSPASRGSLMAAANFLFCFMGLISYHAGRIYKTMKGNRPICAVQVATLPSLILGAGF 443  
 Qy 363 FINFIAIYHASRAIPFGTMVAVCCICFVILPLNLVGTILGNLSGPN-NEPCRVNAV 421  
 Db 444 LLNFLICKHSSGAVPFGTMVALLIMWFICIDMLPLIFLCFYFG--YRKQYHPVTRTNQIP 501  
 Qy 422 RPIPEKKWMEPAVIVCLGILPGSIFITMYFIPTSFWAYKIYVYVGMMLVLVILCIV 481  
 Db 502 RQVPEQPFRLIPSLSLIAGVLPFGAMFIELFFFNATWENQFYFLFGFLFIVSLAIS 561  
 Qy 482 TVCVTVCTIVCYFLLNAEDYRWQWTSFSAASTAIYVYVYFYYFRTKMYGLPQTSFY 541  
 Db 562 TQIYSVATYFSLCAENYRWNRWRSFVSGGSFYVNAVAFYNTKLTIEGFPVTLVFS 621









Db 515 HPYLFMEGFFCGFGLVTTCTIMVSIITVYFQLCSENNWNRSFITPGCGIYVIFSV 574  
QY 522 YYYFFTKMYKGLFQTSFYFGYMAVESFALGIMCGAIGYMGTSFAFVKIYTNVKID 576  
Db 575 FYWFFKISSSLATAVLYFGYLLISLVFLGSGVGFAGFLVKNKIYASIKID 629  
RESULT 10  
S52673  
probable membrane protein YDR107c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YD9727.03c  
C:Species: Saccharomyces cerevisiae  
C:Date: 19-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 19-Apr-2002  
C:Accession: S52673  
R:Murphy, L.; Shore, L.; Harris, D.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S52671  
A:Accession: S52673  
A:Molecule type: DNA  
A:Residues: 1-672 <MUR>  
A:Cross-references: EMBL:Z48758; NID:g747879; PID:g747882; GSPDB:GN000004; MIPS:YDR107c  
C:Genetics:  
A:Gene: MIPS:YDR107c  
A:Cross-references: SGD:S0002514  
A:Map position: 4R  
C:Superfamily: Schizosaccharomyces pombe probable transmembrane protein SPBC1105.08  
C:Keywords: transmembrane protein  
F:311-327/Domain: transmembrane #status predicted <TM1>  
F:384-400/Domain: transmembrane #status predicted <TM2>  
F:408-424/Domain: transmembrane #status predicted <TM3>  
F:444-460/Domain: transmembrane #status predicted <TM4>  
F:479-495/Domain: transmembrane #status predicted <TM5>  
F:536-552/Domain: transmembrane #status predicted <TM6>  
F:561-577/Domain: transmembrane #status predicted <TM7>  
F:618-634/Domain: transmembrane #status predicted <TM8>  
F:640-656/Domain: transmembrane #status predicted <TM9>  
Query Match 21.6%; Score 667.5; DB 2; Length 672;  
Best Local Similarity 25.8%; Pred. No. 6.3e-44;  
Matches 169; Conservative 125; Mismatches 252; Indels 109; Gaps 16;  
QY 21 TYQDKKEVLMNTVGP--YHNQRE-----TYKFSLPFCVGSKKKSISHY 63  
Db 28 TYHSGDEIPLLVKNLTPSIYFQHQDEBNDVSGDKHEFLSYDYKNRPFHCRPEHVEKQ 87  
QY 64 HETLGEALQGVLEFSCLDIKFKDDVNPATYCEIDLDKERDAFVAIKNHYWQMYIDD 123  
Db 88 PESLGSVIFGDIYNSPFQNLMLLEKCEKVALCKSTIPGDKAFINTLIKSGFFQNMLVDG 147  
QY 124 LP-----TWG-----IVGEA-----DENGEDY----- 140  
Db 148 LPAARKAYDSRTKTYNYGTGFGELGFTDVKQTVDGKAVPTMEELTSEASNEVDILDAFLP 207  
QY 141 -----YLWYKKLEIGN--GN-----RIVDVNL-----TSEGVK 168  
Db 208 KVKPNLVKTVLPEYFVNHFDIEVEFHDRGNDRVGVIVNPNVSTERSPPGACSTTGK 267  
QY 169 KLPNTK---IQMSYSVKKKSDVKDEPDKYLDPSFFOHRHWFPSIFNSFMVIFLVG 225  
Db 268 LIIDEDKDNVEYFYSVKFVASDTVWATRWKYL--HIYDPQIQWFSLNFSVIVILLSS 325  
QY 226 LVSMILMRLTKRKYARYSKREEMDDMDRLGDGYGNKQVHGDVFRPSSHPLIFSSLIGSG 285  
Db 326 VMHSLLRALKSLARYNEL----NLDNEFHDSGKWLGHGDVFRTPSKSMLLSILVSGS 381  
QY 286 QITFV---SLIIVIAMIEDLYTERGSMSTAIFVYATSPVNGVFGSGLSARQGRRW 342  
Db 382 MQLFLVMVCSIFFAAVGLVSPV--SRGSLPTVMFVLVYALFGVGYGVSAMGVYKFFRGPYW 439  
QY 343 IKOMFTGAFILIPAMVCGTAFFINFIAYIYHASRAIPEGTMVAVCCICFFVILPLNLVGTI 402  
Db 440 KANNIITPLLGAIFLLIYIMNFFLLFAHSSGVIPARSLFFILLLWFLVSPVLSFAGSI 499

QY 403 LGRNLGQPNFPCRVNAVPRPIPEKKWFMEPAVIVCLGGLPFGSIFIEFYFTSFWAY 462  
Db 500 VAHKQCNDWDEHPTKTNQIARQIPQPMWYLRQAOTLIAGIFSGSLAVELYFYVSSLWFN 559  
QY 463 KIYYVGVFMMVLVLIVLCIVTCVTVCTYFLLNAEDYRWQWTSF--LSAASATAIYVVMYSF 521  
Db 560 KIFMFGFLFLSLLLTATLSLTILTYISLGLNNLWQWRSFIITGGLGCSYTFIHSI 619  
QY 522 YYVFEKTKMYGLFQTSFYFGYMAVESFALGIMCGAIGYMGTSFAFVKIYTNVKID 576  
Db 620 --LFTAKLGGVITVVLVLYLGLYSIISALCCVVTGAIGFFSSMFFIRKIYSAIRKE 672  
RESULT 11  
H85135  
hypothetical protein AT4g12650 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001  
C:Accession: H85135  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp  
Nature 402, 769-777, 1999  
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: H85135  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-527 <STO>  
A:Cross-references: GB:NC\_001268; NID:g7267967; PIDN:CAB78308.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: AT4g12650  
A:Map position: 4  
Query Match 21.0%; Score 650; DB 2; Length 527;  
Best Local Similarity 32.8%; Pred. No. 1.1e-42;  
Matches 160; Conservative 91; Mismatches 171; Indels 66; Gaps 17;  
QY 128 GIVGEADENGEDYILWYKKLEIGN--GNRIY--DVNLTSEGVKVL-----VPNT---- 174  
Db 67 GVISEAD-----KKKALGYEIVGVFEVPCSVKYDAEKMTKLHMYDPPVSNCP 115  
QY 175 -----KIOMSYSVKKKSDVKFEDFDKYLDPSFFOHRHWFPSIFNSFMVIF 222  
Db 116 ELDKAQIIEKHEHRTFTEYEFVKSETRPWRDAVL--KMEGARVHWFSLNSLAWIFF 173  
QY 223 LVGLVSMILMRLTKRKYARYSKREEMD----DMDRLGDGYGNKQVHGDVFRPSSHPLI 277  
Db 174 LAGIVFVIFLRTVRRDLTKY---EELDKAQAOQNEELS---GWKLVGVDVFRPEMSKL 227  
QY 278 FSSLIGSGCQIFAVSLIIVIAMIEDLY--TERGSMSTAIFVYATSPVNGYFGGSLYAR 336  
Db 228 LCIMVGDGVRIETGMVAVTVIVFAALGFMSPASRGMLLTGMILYFLGIVAGYAGVLRWT 287  
QY 337 QGG--RRWIKQMFIGAFLIPAMVCGTAFFI-----NFTAIYYHASRAIPEGTMVAVCCICF 390  
Db 288 VKGTSEGRWSLSIACFFP---GIAFVLLTVLNFLLWSSNSTGAIPISLYFELLALWF 343  
QY 391 FVTLPLNLVGTIILGRNLGQPNFPCRVNAVPRPIPEKKWFMEPAVIVCLG--GILPFGSIF 449  
Db 344 CISVPLTLFGFGFLGTAREA--IQPVRTNQIPREIPERKY---PSWLLVLGAGILPFGTLF 399  
QY 450 IEMYFTSFWAYKIYYVGVFMMVLVLIVLCIVTCVTVCTYFLLNAEDYRWQWTSFSLA 509  
Db 400 IELFFIFSSILWGREYVYVFGFLVLVLLLVVCAEVSVLTYMHLCVDEWRWNWKAIFYAS 459  
QY 510 ASTAIYVVMYSFYFFYFVKTK--WYGLFQTSFYFGYMAVESFALGIMCGAIGYMGTSFAVRK 568  
Db 460 GSVALLYFAIYSINLYVFDLQSLGSPVSAIMLYIGYSLLMAITATLATGTGTLGFLTSFYFVHY 519  
QY 569 IYTNVKID 576  
Db 520 LFSSVKID 527

## RESULT 12

H86280  
protein F10B6.2 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: H86280  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H86280  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-260 <STO>  
A:Cross-references: GB:AE005172; NID:g8778207; PIDN:AAF79216.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F10B6.2  
A:Map position: 1

Query Match 14.5%; Score 447; DB 2; Length 260;

Best Local Similarity 36.2%; Pred. No. 2.7e-27;  
Matches 87; Conservative 53; Mismatches 86; Indels 14; Gaps 5;

QY 14 RADEHEHTYQDKKEVVLMMNTVGPYHNRQTYKYFSLPCVGVSKKSTISHYHETLGEALQG 73

DB 23 RSDASDRHYKEGDTVPLANKVGFPHNPSETRYFDLPFCI--PEGVKEKKEALGEVLNG 80

QY 74 VELEFSGLDIKFKDDVMPATYCEIDLDKRDFAVYAKNHVYQMYIDDLPTWIGVGEA 133

DB 81 DRLSVAPYKLNFRDESEVYCNKLSKEVKQFRKAVEKDYFQMYDDLPWGFPGKV 140

QY 134 DENGED-----YLYWTKYKKLGFGNGNRIVDVN--LTSEGVKVKLPVNTKI--OMSYSVK 183

DB 141 DKDIKSDPSEFYKFLYKHQFELYKRWKRVIEISARMOPHSULVDLTEDKREVDAEFYTKV 200

QY 184 WRKSDVKFEDFDKYLDPSPFFQH--RIHWFSEFNSFMWVFLVGLVSMILMRLRKDYAR 241

DB 201 WKETETPEKRMKEKYSMSSSLPHLEHWFSEIINSCVTYVLLLTGFLATILMRVLYKNDPMK 260

## RESULT 13

S50616  
hypothetical protein YER113c - yeast (Saccharomyces cerevisiae)  
C:Species: Saccharomyces cerevisiae  
C:Date: 28-May-1993 #sequence\_revision 24-Feb-1995 #text\_change 19-Apr-2002  
C:Accession: S50616  
R:Dietrich, F.S.  
submitted to the EMBL Data Library, December 1994  
A:Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda  
A:Reference number: S50437  
A:Accession: S50616  
A:Molecule type: DNA  
A:Residues: 1-706 <DIE>  
A:Cross-references: EMBL:U18916; NID:g1384128; PID:g603352; GSPDB:GN00005; MIPS:YER113c  
C:Genetics:  
A:Gene: MIPS:YER113c  
A:Cross-references: SGD:S0000915  
A:Map position: 5R

Query Match 14.2%; Score 438; DB 2; Length 706;

Best Local Similarity 24.9%; Pred. No. 4.5e-26;  
Matches 157; Conservative 98; Mismatches 269; Indels 106; Gaps 21;

QY 42 QETKYKFSLPFCVGVSKKSTISHYHETLGEALQGVLEFSGLDTKFKDDVMPATYCEIDLK 101

DB 76 QLPYAYVDLPFTCPPTMHKKPLHLSEIIRGDRKWESYKLRFGEDNPCTILCARCTK 135

QY 102 EKRDADFVYATKNHYWQMYIDD-LPIWGI-----VGEADENGEDYILWT 144

DB 136 EGMOTLDKLVREGYVVOVWLIDDELPAATFTISTDHHKKYVASGFPGLGFDIDPDQDKTYLHN 195

QY 145 YKLEIGFNG-----NRIVDNVTSE-----GKVK-----LVPN-----TKIQMS 179

DB 196 HVMLVIRFHASDNDKNTIVGFYPRSVSDYHCPGASKNYEQYEVIPEDENELTYLPFT 255

QY 180 YSVKWKKS-DVKEDEPRDKYLDSPFOH-----RIHWFSEFNSFMWVFLVGLVSMILMRT 234

DB 256 YSYWREEFEEFVNNHWDYFLNAGELSDQSIQFHWMSLANSVGLVLSIFITLIIVRV 315

QY 235 LRKDYARYSKEEM-----DDMDRLGDYGNKKQVHGDFV---RPSSHPL-IFSSL 281

DB 316 MYTDKSNKSPKYMINEGTEIEDDDDDDDKYGKYSVYTVAKDWIQNGRPNLGLKVLILL 375

QY 282 IGSQCQ-IFAVSLIIVIAMIEDLYTERGSMNSTAIFVYAATSPVNGYFGGSLYARQ--- 337

DB 376 VSEGVQFLFTIGSLRTISCSMNKLHNVRNSVLTMAILFF-----VLGAFNASFVGTRLSM 430

QY 338 -----GGRWIK--QMPIGAFLI-----PAMVCGTAFFINFIAIYYHASRAI 377

DB 431 VTKTKRTKANYLDDNRYLDKDKKFSPTFTILCGSSLPGLVWVSTFLNSIWAHDSTSA 490

QY 378 PFGTMVAVCCICFFVILPLNLVGTILGN-----LSGQNPFCRVNAVPRPIPEKKWF 430

DB 491 PKRTIVFMSIYFIVCLPLSGGIANNIPLOPYWLSGITKDESNSDGNGLFVPSRAK 550

QY 431 MEPAVI--VCLGILPFGSIFIEYFIFTSFWAYK--IYVYVGFMMVLVLVILCIVTVCVT 486

DB 551 FNLVYCGVILCGFLLPLVIVVEMQYVYKSLWEKTFYFYVGFLLSILLCVLMEIS 610

QY 487 IVCTYFLN--AED---YRWQTSFLSAASTAIYVVMYSFYFFYFKTKMYGLFQTSFYF 540

DB 611 IIGSYLLMRFCEFDKVVVRNNRWKCFEMGFGVGMELYSLYIFAFLNIHGFSSILISI 670

QY 541 GYMAVESTALGIMCGAIGYMGTSAFVRKIY 570

DB 671 CYSLIFNVMSLGLGALSULTASWFKIY 700

RESULT 14

H95240

conserved hypothetical protein SP2057 [imported] - Streptococcus pneumoniae (strain T

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001

C:Accession: H95240

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappl

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: H95240

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-605 <GR>

A:Cross-references: GB:AE005672; PIDN:AAK76121.1; PID:g14973568; GSPDB:GN00164; TIGR:

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP2057

Query Match 3.9%; Score 121; DB 2; Length 605;

Best Local Similarity 19.9%; Pred. No. 0.16;

Matches 83; Conservative 59; Mismatches 116; Indels 160; Gaps 22;

QY 207 RIHWFSEFN-----SFMWVIFLVG-----LVSMILMRLRKDYARYS 243

DB 2 RIKWFLIRIIGLLVLLVHFFQTFIPGPGFVDVFTFGSLITALLIE-----EFS 54

QY 244 KEEMDDMDRLDGEYGMKQVHGDVFRPSHPLI-----FSSLI-----GSG 285  
Db 55 KNEIDLII-----GFERRRFYRIVPPVLMVLVMTPEFTLVQRQDYVAGIG 99  
QY 286 CQI-----FAVSLIIVIIV-----MIEDLYTERGSM-----STAFVYAATSPV 325  
Db 100 GQIAGVLGEMTNFYELLTGGSYESQIPHLFVHNWSLAVEHYIILWGLAVWFLSKQAKS 159  
QY 326 NGYFGGSLYAROGGRWIK--OMFIGAFILIPAMVCGTAFFINFIAIYYHASRAIPF--GT 381  
Db 160 NGQLKGMVFLLSAVAFILISFFSMFIGSLVTSY--SSVYFSSLTHVY-----PFFLGS 210  
QY 382 MVAVCCICFFVILPLNLVG---TILGRNLSQPNPCRVNAVPRPIPEKKWFMEMPATIV 437  
Db 211 MLA-----TIVGVRQTSLVKQL-----DKIWDLRKTLVV 240  
QY 438 CLGGILPGSIFIEYFI-FTSFNAYKIYYVGFMMVLVILCIYVCTIVCTYFLLNA 496  
Db 241 FGGG---FGFLVLLTFPVKFTYLFAYLI---GFLASLAALAMILAA-----RVLHE 286  
QY 497 EDIRWQWT---SFLSAATAIYVYMYSFYFFKTK-----MYGLFQTSFY 539  
Db 287 KTHHIQESKIISFLADTSYAVILFHWPFYIIFSOLTSNLLAVLLTLCISYGFASLSFY 344

RESULT 15  
A99705  
hypothetical protein spr1868 [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C:Accession: A99705  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E  
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: A99705  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-605 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAL00670.1; PID:gl5459558; GSPDB:GN00174  
C:Genetics:  
A:Gene: spr1868

Query Match 3.9%; Score 121; DB 2; Length 605;  
Best Local Similarity 19.9%; Pred. NO. 0.16;  
Matches 83; Conservative 59; Mismatches 116; Indels 160; Gaps 22;

QY 207 RIHWFSIFN-----SPMMVIFLVG-----LVSMLMRTLKDYARYS 243  
Db 2 RIKWFSIRIIGLLVLYHFFQIPGGFGVDVFFFTSGFLITALLIE-----EFS 54  
QY 244 KEEMDDMDRLDGEYGMKQVHGDVFRPSHPLI-----FSSLI-----GSG 285  
Db 55 KNEIDLII-----GFERRRFYRIVPPVLMVLVMTPEFTLVQRQDYVAGIG 99  
QY 286 CQI-----FAVSLIIVIIV-----MIEDLYTERGSM-----STAFVYAATSPV 325  
Db 100 GQIAGVLGEMTNFYELLTGGSYESQIPHLFVHNWSLAVEHYIILWGLAVWFLSKQAKS 159  
QY 326 NGYFGGSLYAROGGRWIK--OMFIGAFILIPAMVCGTAFFINFIAIYYHASRAIPF--GT 381  
Db 160 NGQLKGMVFLLSAVAFILISFFSMFIGSLVTSY--SSVYFSSLTHVY-----PFFLGS 210  
QY 382 MVAVCCICFFVILPLNLVG---TILGRNLSQPNPCRVNAVPRPIPEKKWFMEMPATIV 437  
Db 211 MLA-----TIVGVRQTSLVKQL-----DKIWDLRKTLVV 240  
QY 438 CLGGILPGSIFIEYFI-FTSFNAYKIYYVGFMMVLVILCIYVCTIVCTYFLLNA 496  
Db 241 FGGG---FGFLVLLTFPVKFTYLFAYLI---GFLASLAALAMILAA-----RVLHE 286

QY 497 EDIRWQWT---SFLSAATAIYVYMYSFYFFKTK-----MYGLFQTSFY 539  
Db 287 KTHHIQESKIISFLADTSYAVILFHWPFYIIFSOLTSNLLAVLLTLCISYGFASLSFY 344

Search completed: January 20, 2003, 14:36:44  
Job time : 54 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	950.5	30.8	642	9	US-10-201-964-1		Sequence 1, Appli
2	674	21.8	125	10	US-09-915-582-52		Sequence 52, Appl
3	674	21.8	125	10	US-09-915-582-68		Sequence 68, Appl
4	130.5	4.2	351	10	US-09-820-893-114		Sequence 114, App
5	119.5	3.9	58	10	US-09-864-761-34915		Sequence 34915, A
6	119.5	3.9	58	10	US-09-864-761-36367		Sequence 36367, A
7	117.5	3.8	307	10	US-09-820-893-119		Sequence 119, App
8	117.5	3.8	322	10	US-09-820-893-117		Sequence 117, App
9	114	3.7	234	9	US-10-001-857-176		Sequence 176, App
10	108.5	3.5	433	9	US-09-738-626-6716		Sequence 6716, Ap
11	106	3.4	1681	10	US-09-920-653-3		Sequence 3, Appli
12	104.5	3.4	445	9	US-09-738-626-3627		Sequence 3627, Ap
13	104.5	3.4	822	10	US-09-824-734-3		Sequence 3, Appli
14	104	3.4	385	9	US-09-738-626-4559		Sequence 4559, Ap
15	104	3.4	791	9	US-09-738-626-4530		Sequence 4530, Ap
16	102	3.3	609	10	US-09-801-368-50		Sequence 50, Appl
17	101.5	3.3	305	10	US-09-815-242-13291		Sequence 13291, A
18	101.5	3.3	305	10	US-09-815-242-13553		Sequence 13553, A
19	101.5	3.3	3092	10	US-09-801-368-172		Sequence 172, App





Db 121 LYLQ--RQY-----IPVKMSKAEWIEFWAYMY-----VGSLVVILCLS 160  
QY 390 FVLPLNLVGTILGRNLG--OPN-----FPC--RVN---AVPR 422  
Db 161 FFLSSWDFIPAVYGFILSVDDTPNIGLWYFFAEHFSLFVFCVFOINVFFYTIPL 220  
QY 423 PIPEKK-----WFEPAVIVCLGILPFGSIFIEYFIPTSFWAYKIYVYVGFMLVLVI 477  
Db 221 AIKLKEPIFFMFQIAVIAIFKSYPTVGD--VALYMAFFPVW---NHLRYELRNIEVL 274  
QY 478 LCIVTVCVTVICHYFLLNAEDYRWQWTSFLSAASTAIY-----VVMYGFYFFFK 527  
Db 275 TCIIIVCSLFFPLVHL-----WIYPGNANSFFYAITLTFNVGQILLISDYFAFL 326  
QY 528 TKMY----GLFQTS 537  
Db 327 RREYILTHGLYLA 340

RESULT 5  
US-09-864-761-34915  
; Sequence 34915, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-x-1  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 34915

LENGTH: 58  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
; OTHER INFORMATION: MAP TO AL049539.16  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.1  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.2  
; OTHER INFORMATION: EST\_HUMAN HIT: AW372226.1, EVALUE 1.00e-30  
; OTHER INFORMATION: SWISSPROT HIT: P32802, EVALUE 2.00e-05  
US-09-864-761-34915

Query Match 3.9%; Score 119.5; DB 10; Length 58;  
Best Local Similarity 43.6%; Pred. No. 0.00042;  
Matches 24; Conservative 9; Mismatches 21; Indels 1; Gaps 1;  
QY 377 IPFGTWAVCCICOFFVILPLNLVGTILGRNLGSGPNFPCRVNAVPRPIPEKKWFM 431  
Db 1 VPFTMVALLCMWFGISLPLVLGYVFGFRKQPYDN-PVRTNQIPIROIPEQRWYM 54  
RESULT 6  
US-09-864-761-36367  
; Sequence 36367, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO  
; FILE REFERENCE: Aeomica-x-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687

Query Match	3.8%;	Score 117.5;	DB 10;	Length 307;
Best Local Similarity	23.5%;	Pred. No. 0.0054;		
Matches	58; Conservative 38;	Mismatches 80;	Indels 71;	Gaps 14;
QY	277	IFSSLIGSGCOIPAVSLIVIIIVAMIEDLYTERGSMLSIAFV----	YAATSPVNQYEFGS	332
		:           :           :		
Db	67	ILSCVAKSTCAI--NNTLIATFI-----LTTIKGSAFSLAIFALATYQSLLPVLTFVPGL	120	
		:           :           :		
QY	333	LYARQGGRWIKOMFIGAFILIPAWCVGTAFPI---NFITAIYHSAIRATPFCTMVAVCCIC	389	
		:           :           :		
Db	121	LXLLQ--RQY-----IPVKMKSKAPWFSEWYAMMY-----VGSLVIIICLS	160	
		:           :           :		
QY	390	FFVILPLNLVGTILGRNLG-----OPN-----FPC--RVN-----AVPR	422	
		:           :           :		
Db	161	FFLLSSMDFTIPAVYGFTLSVPDPTPNIGLEFWYFAEMFEHFSFLFCVCVFQINVFYTIPL	220	
		:           :           :		

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Query Match      3.8%;  Score 117.5;  DB 10;  Length 322;
Best Local Similarity 23.5%;  Pred. No. 0.0058;
Matches 58;  Conservative 38;  Mismatches 80;  Indels 71;  Gaps 14;

QY 277 IFSSLIGGCOIFAVSLIIVIAMIEDLYTERGSMLSAIFV-----YAATSPVNGYFGGS 332
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 82 ILSVANSTCAI--NNTLIAFTI-----LTTIKGSAFLSAIFALALATYQSLYPLTLFVPEGL 135
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 333 LYAROGGRWTKQMFIGAFLIPAMVCGTAFTI---NFTAIYYHASRAIFPGTMVAVCCIC 389
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 136 LYLLOQ--ROY-----IPVKMKSAFIFSWWEYAMMY-----VGSLLVVIICLS 175
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 390 FFVILPLNLVGTILGRNLSG--OPN-----PPC--RVN-----AVPR 422
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 176 FFLSSWDFIPAVYGFILSPDLPTNIGLFWYFAEMFEHSLFVFCVQFNVEFYTIPL 235
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 423 PIPEKK-----WFMEPAVIVCLGILPFGSIFIEMYFIFTSFWAYKIYVYGFMMMLVLI 477
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 236 AIKLKEHIPFMFIQIAVIAIFKSPYVGD--VALYMAFFPVW---NHLRYFLRNIFVL 289
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 478 LCIVTVC 484
    | | | |
Db 290 TCIIVC 296
    | | | |

RESULT 9
US-10-001-857-176
; Sequence 176, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20

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Db 1352 --RVIIHILRPGKPKVPHDMLP-LILALPALLNISLILFLVMFVIAIFGMYNFAYVKE 1408

QY 468 -----YGFMMVL 475  
 Db 1409 AGINDVSNFTFGSSMLCL 1427

RESULT 12

US-09-738-626-3627  
 ; Sequence 3627, Application US/09738626  
 ; Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI  
 APPLICANT: MIZOGUCHI, HIROSHI  
 APPLICANT: ANDO, SEIKO  
 APPLICANT: HAYASHI, MIKIRO  
 APPLICANT: OCHIAI, KEIKO  
 APPLICANT: YOKOI, HARUHIKO  
 APPLICANT: TATEISHI, NAKO  
 APPLICANT: SENO, AKIHIRO  
 APPLICANT: IKEDA, MASATO  
 APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738,626  
 ; PRIOR FILING DATE: 2000-12-18  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: PatentIn ver. 3.0  
 ; SEQ ID NO 3627  
 ; LENGTH: 445  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum

US-09-738-626-3627

Query Match 3.4%; Score 104.5; DB 9; Length 445;  
 Best Local Similarity 19.6%; Pred. No. 0.13;  
 Matches 57; Conservative 55; Mismatches 116; Indels 63; Gaps 13;

QY 197 KYLDPSFFOHRHWFSEIFSMFVFLVGLVSMILMRLTKDYARVYSKEEEMDDMDRLG 256  
 Db 171 QVNLTFYE--TLUVS-----LVLVIG--SLIALGVKERRGRPLVANPDVQKTLG 220

QY 257 DEYGRQVHGDPVPPSSHPLIFSSLGSCQIFAVSLIIVAMI-EDLYTERGSMISTA 315  
 Db 221 Q--GFKLRND-----RRARFVYIIRTINSIPTYAMAVFFSFDDDLKQWLSFELILT 272

QY 316 IFVYATSPVNGVFGGSLVARQGRRIKQMTGAFELIPAMVCGTAFFNFIAIYHSHR 375  
 Db 273 TWIYAVNLPFNPF--GSFGRHG---WARTVFWGSGIGGAVTLALVYFIPMGVQAGMSN 328

QY 376 AIPFGTMVAVCCICFFVILPLNLVGTILGRNLG-QPNFPCRVNAVPRPIPEKKWMEPA 434  
 Db 329 GVVFGLTIA-----AGALFGVSLAGFVPLSAIAVSLDPK-----HFG 365

QY 435 VIVC-----LGGILPRGSIFIEMYFTSFWAYKIYVYGFMMVLVILCI 480  
 Db 366 AAMATYNLGVGAVGAVGLLVAVF-----HPLIGPTGLILVMIAL 405

RESULT 13

US-09-824-734-3  
 ; Sequence 3, Application US/09824734  
 ; Patent No. US20020083485A1

GENERAL INFORMATION:

APPLICANT: ZHU, JIAN-KANG  
 APPLICANT: SHI, HUAZHONG  
 APPLICANT: ISHITANI, MANABU

APPLICANT: STEVENSON, BECKY  
 ; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS  
 ; FILE REFERENCE: 205644US20  
 ; CURRENT APPLICATION NUMBER: US/09/824,734  
 ; CURRENT FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: US 60/194,648  
 ; PRIOR FILING DATE: 2000-04-04  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 822  
 ; TYPE: PRT  
 ; ORGANISM: Cricetus griseus  
 US-09-824-734-3

Query Match 3.4%; Score 104.5; DB 10; Length 822;  
 Best Local Similarity 20.4%; Pred. No. 0.28;  
 Matches 92; Conservative 64; Mismatches 125; Indels 169; Gaps 23;

QY 213 IFNSEMMVIFLVGLVSMILMRLTKD-----YARYSKEEEMDDM-----DR 253

Db 16 IFPSLLVVVALVGLLPLVLRSHGLQSPSTANTIRCAEPPRERSIGDVTAPSEVPHDDR 75

QY 254 DLGD---EYGWKQVHGDVFRPSSHPLI-----F 278

Db 76 NLTNLHIEHGAKTLR-----KAPVLDIDYLVHRTPFELISWILLACLMLKIGFHVPTI 129

QY 279 SSLIGSCQIFAVSLIIVAMIEDLYTERGSMISTAIFYAATSPV---NGYFGGSLVA 335

Db 130 SSVIPESCLLVVGLLV--GGLIGV-GETPPFLDQVFFLLPPIILDAGYF---LPL 183

QY 336 ROGRRWIKQMFIGAFIPAMVCGT---AFFINFIAIYVHASRAIPFGTMVAVCCICFFV 392

Db 184 RQFTEN-----LGTILIFAVV-GTLWNAFFLG-----GLLYAVCLVGGEQ 222

QY 393 IPLNLVGTILGRNLGQPNFPCRVNAVPRPIPEKKWMEPAVIVC-----LGGIL 443

Db 223 INNIGLDTLL-----FGSIISAV-----DPVAVAVFEEIHINELLHIL 262

QY 444 PEG-----SIFIEMVFIETSFWAYKIYV---YGFMMVLVILCIVTCVIVCTYFL 493

Db 263 VFGEESLNDVAVTVLVHLFEFANYDSIGISDIFLGFVFFVVALGVFVG---VYG 318

QY 494 LNAEDYRWQWTSFLSAATAIYVMSFYVFFKTKMYGLFQTSFYFGYMAVSTALGIM 553

Db 319 IAA--FTSFTSHIRVIE-PLFVFLYS-----YMAVLSAELFHL 354

QY 554 CGAIGYMGTSFAFVR-----KIYTNVK 574

Db 355 SGIMALIASGVVMRPVVEANISHKSHTTIK 384

RESULT 14

US-09-738-626-4559  
 ; Sequence 4559, Application US/09738626  
 ; Publication No. US20020197605A1

GENERAL INFORMATION:

APPLICANT: NAKAGAWA, SATOSHI  
 APPLICANT: MIZOGUCHI, HIROSHI  
 APPLICANT: ANDO, SEIKO  
 APPLICANT: HAYASHI, MIKIRO  
 APPLICANT: OCHIAI, KEIKO  
 APPLICANT: YOKOI, HARUHIKO  
 APPLICANT: TATEISHI, NAKO  
 APPLICANT: SENO, AKIHIRO  
 APPLICANT: IKEDA, MASATO  
 APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738,626  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16

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: PRIOR APPLICATION NUMBER: JP 00/159162
: PRIOR FILING DATE: 2000-04-07
: PRIOR APPLICATION NUMBER: JP 00/280988
: PRIOR FILING DATE: 2000-08-03
: NUMBER OF SEQ ID NOS: 7059
: SOFTWARE: PatentIn ver. 3.0
: SEQ ID NO 4559
: LENGTH: 385
: TYPE: PRT
: ORGANISM: Corynebacterium glutamicum
: US-09-738-626-4559

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Query Match	3.4%;	Score 104;	DB 9;	Length 385;	
Best Local Similarity	20.9%;	Pred. No. 0.12;			
Matches	62;	Conservative 50;	Mismatches 118;	Indels 66;	Gaps

  

QY	210	WFSIFNSFMVIFVLGVLSMILMRTLRKDYARYSKEEEMDDDDRRDLGDEYQKQVHGVDVF	269
		:    :   : :   :	
Db	82	FFSILSIAPAVLLGVYSVITIFLA-----SDSTEILNLVRDEVNQY-----Vp 123	
QY	270	RPSHPHL- -IFSSILSGCGQIFAVSLIVIVAMIEDLYTERGSMSTALFVYAATSPVNG	327
		:    :    :	
Db	124	EDOSHVVNGVIDSIAGS-----AAGQGVAVGVITALT-----SSAIVRAFSCAN- 171	
QY	328	YFGGSLYAROGRRWTKOMFIGAFLIPAMVCGTAFTINFIAIYVYHASRAIPETGMVAVCC	387
		: :         :    :    :	
Db	172	----AVYGRSEGRTLKRWMLLFNLALLG-----IIILVSWLNETFLVMGIFAPIA- 222	
QY	388	ICFVFLPILNLVGTILGRNLSGP-----NFPGRVNAV-----PRPIEKKWFM 431	
		:   :   :	
Db	223	-----EPLHLTNVLSFLTDREMPIWIWRFPVGVGLIMEFATLYYVWAPNARPKFRL 276	
QY	432	EPAVIVCLGGILPFGSIFTEMVFYFTSWAYKIYYVYGFMMILVLVILCIIVTCVTI	487
		:     :     :     :     :	
Db	277	SLGSLFIAIVGILLAG---VGLNPFYFTLFAAFSSYGAVGSLLAVFTALWVFNICLII 329	

RESULT 15

```

US-09-738-626-4530
; Sequence 4530, Application US/09738626
; Publication No. US20020197605A1
;
; GENERAL INFORMATION:
;
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
;
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
;
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
;
; NUMBER OF SEQ ID NOS: 7059
;
; SOFTWARE: PatentIn ver. 3.0
;
; SEQ ID NO 4530
;
; LENGTH: 791
; TYPE: PRT
;
; ORGANISM: Corynebacterium glutamicum
;
; US-09-738-626-4530

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Query Match 3.4%; Score 104; DB 9; Length 791;  
Best Local Similarity 22.6%; Pred. No. 0.3;  
Matches 65; Conservative 39; Mismatches 115; Indels 68; Gaps 12;

Qy	225	GLVSMILMRTLKDYARYSKE-----EEMDDMRDL-----GDGYGKWQVHGVD-----	268
		:	
Db	160	GIISMTFADASMDISAEDEKVTNLTDEYDDGDLTVVNGNVFGAAATSLDSTSELIGL	219
		:	
Qy	269	-----FRPSHPLIFSSLLIGSCQIFAYFVSLIIVAMTEDLYTERGSMLSFTA	315
		:	
Db	220	LVAAVLVITVFGSFIAGMPLI-SAIIGVGIGITMGITOLATAFTDSVNDMTPTLASMIGLA	278
		:	
Qy	316	IFVVAATSPVNGVFGGSLYARQG-----GRRWIKOMFTGAFILIPAM	356
		:  :	
Db	279	VGIDYALFVYS-RFRNELISQTDANDLEPKELAERLTWPAAARAHAMGNVAGTAGSAVV	337
		:	
Qy	357	VGCTAPFPIFIATVYHASRAIPGTTWAVCC-----ICFFVTLPLNLTGTTILGRNLSQPNF	413
		:	
Db	338	FAGTTVLIALVAL---SIINIPELTVNAIAAATVAIAVLVAUSFFLALLG--LLGTRIF	392
		:	
Qy	414	PCRVNA--VPRPIPEK-----KW-----FMPEPAVIVCLGGILPFGSIFI	450
		:	
Db	393	AARVPGPKVPDPEDEKPTMGLKWLVRVRKMPVAYLLGVVLLCAIAI	439
		:	

Search completed: January 20, 2003, 14:15:02  
Job time : 251 secs



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OM protein - protein search, using sw model

Run on: January 20, 2003, 10:32:24 ; Search time 37 seconds  
(without alignments)  
458.043 Million cell updates/sec

Title: US-09-319-724A-14

Perfect score: 3089

Sequence: 1 AALWLLLLLPRTTRADEHEH.....IGYMGTSFAVRKIYTNVKID 576

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCFUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	950.5	30.8	625	US-08-959-004-10	Sequence 10, Appl
2	843.5	27.3	663	US-08-959-004-5	Sequence 5, Appl
3	694	22.5	667	US-08-959-004-11	Sequence 11, Appl
4	118.5	3.8	496	US-09-134-001C-3703	Sequence 3703, Ap
5	112.5	3.6	237	US-09-134-001C-3057	Sequence 3057, Ap
6	107.5	3.5	408	US-08-742-440A-6	Sequence 6, Appl
7	107	3.5	333	US-09-576-160B-6	Sequence 6, Appl
8	104.5	3.4	453	US-08-439-131A-5	Sequence 5, Appl
9	104.5	3.4	453	US-08-440-674-4	Sequence 4, Appl
10	101.5	3.3	2938	PCT-US94-00198-3	Sequence 3, Appl
11	99.5	3.2	616	US-08-149-100-2	Sequence 2, Appl
12	97.5	3.2	470	US-08-724-394A-10	Sequence 10, Appl
13	96	3.1	357	PCT-US95-07180-3	Sequence 3, Appl
14	95	3.1	367	US-08-514-451A-7	Sequence 7, Appl
15	94.5	3.1	425	US-08-313-553-13	Sequence 13, Appl
16	94.5	3.1	425	US-08-767-993-13	Sequence 13, Appl
17	94.5	3.1	503	US-09-134-001C-3096	Sequence 3096, Ap
18	94	3.0	360	US-08-875-573-20	Sequence 20, Appl
19	94	3.0	360	US-09-232-878-2	Sequence 2, Appl
20	94	3.0	360	US-09-045-583-55	Sequence 55, Appl
21	94	3.0	360	US-09-534-185-55	Sequence 55, Appl
22	94	3.0	1873	US-08-336-257A-7	Sequence 7, Appl
23	93	3.0	434	US-08-677-049-7	Sequence 7, Appl
24	92.5	3.0	521	US-09-134-001C-4290	Sequence 4290, Ap
25	92.5	3.0	844	US-09-422-936-51	Sequence 51, Appl
26	92.5	3.0	886	US-09-422-936-77	Sequence 77, Appl
27	92.5	3.0	892	US-09-422-936-75	Sequence 75, Appl

28	92.5	3.0	899	4	US-09-422-936-71	Sequence 71, Appl
29	92.5	3.0	961	4	US-09-422-936-49	Sequence 49, Appl
30	92.5	3.0	1076	4	US-09-134-001C-4037	Sequence 4037, Ap
31	91.5	3.0	409	4	US-09-326-203A-23	Sequence 23, Appl
32	91	2.9	464	4	US-09-724-864-40	Sequence 40, Appl
33	91	2.9	606	3	US-08-620-077B-3	Sequence 3, Appl
34	90.5	2.9	486	4	US-09-134-001C-3593	Sequence 3593, Ap
35	90	2.9	352	4	US-09-576-160B-1	Sequence 1, Appl
36	90	2.9	352	4	US-09-576-160B-2	Sequence 2, Appl
37	90	2.9	360	4	US-08-833-752-10	Sequence 10, Appl
38	90	2.9	473	1	US-08-439-131A-4	Sequence 4, Appl
39	90	2.9	473	1	US-08-440-674-3	Sequence 3, Appl
40	90	2.9	1240	3	US-08-930-996A-4	Sequence 4, Appl
41	90	2.9	1873	1	US-08-435-675B-4	Sequence 4, Appl
42	89.5	2.9	411	4	US-08-887-534A-80	Sequence 80, Appl
43	89.5	2.9	844	4	US-09-422-936-47	Sequence 47, Appl
44	89.5	2.9	960	4	US-09-422-936-45	Sequence 45, Appl
45	89	2.9	464	4	US-09-604-978-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1  
US-08-959-004-10  
; Sequence 10, Application US/08959004  
; Patent No. 6197543  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Kaser, Matthew  
; TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/959,004  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0414 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 625 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1665777

US-08-959-004-10

Query Match 30.8%; Score 950.5; DB 4; Length 625;  
Best Local Similarity 35.7%; Pred. No. 6.6e-85;  
Matches 214; Conservative 100; Mismatches 212; Indels 73; Gaps 11;  
QY 42 QETKYKSLPFCVGSKKSISHYHETLGEALOGVELEFSGLDIKFKDDVMPATYCE-----WGI-VG 131  
DB 36 QLPVEYSLPFCQPSK--ITYKAENLGEVLGRDVRTPFQVLMNSEKKCEVLCSQSNKP 93  
QY 97 IDLDKERDAFVAIAKHNHYOMYIDPLI-----WGI-VG 131  
DB 94 VTLVEOSRLVAERITEDIYVHLIADNLPVATRLLEYLSNRDSDKKKEKDVQFEHGVRLG 153  
QY 132 EAD-----ENGEDYILWYK--KLEIGFNGNRIVDNLTSEGVKVLV 171  
DB 154 FTDVWKIYLHNHLSFILIYHREDMEEDQEHYVRVREVIPOSLRLEDLKADEKSSCTLP 213  
QY 172 PNT-----KIQMSYSVKKKSDVKPFEDRKYLDPFSFQHRHWFHSIFNSFM 218  
DB 214 EGTNSSPOEIDPTKENQLYFTYSVHWEESDIKWAASRWDYLTMSDVQ--IHWFSIINSVV 271  
QY 219 MVFLVCLVSKMLMRLTKOYARYSKKEEMDDMDRLGDEYGHQVGHGVFRPSSHPFLIF 278  
DB 272 VWFPLSGILSMIITIRLKDIANYNKEDDIE---DTMEESGWKLVHGQVFRPQYPMIL 327  
QY 279 SSLIGSCQIFAVSLIIVIAMIEDLY-TERGSMLSIAFYAATSPVNGYFGGSLYARQ 337  
DB 328 SSLGSGIQIFCMILIVFVAMLGMLSPSRGALMTTACFLPMFGVFGFSAGRLYRTL 387  
QY 338 GGRWIKOMFIGAFLPAMVCGTAFFINFAIYHSAIRAIPTGTMAVCCICFVILPLN 397  
DB 388 KGRWKKGAFTATLPVGVVFGICFVLCNCFIMCKHSSGAVPPTMVALLCMFGISLPLV 447  
QY 398 LVGTILGRNLSGQNPFCRVNAPRPIPEKKWFEPNAVIVCLGILPFGSIFTEMFIET 457  
DB 448 YLGYGFRKQPDYD-VPRTNQIPROIQEORWYNNRNVFGILMAGILPFGAMFTELPFIS 506  
QY 458 SFWAYKIYVYVGMVLVLVILCIIVTCVTIVCTYFLLNAEDYRWQWTSFLSAASTAIYVY 517  
DB 507 AIWENQFYLLFGFLFVILVSCQISIVMYVQLCAEDYRWWRNFLVSGSFAFYVL 566  
QY 518 MYSEYFFTKMYGLFQTSFYGYMAVFTALGICGAIGYMGTSFAVRKIYTNVKID 576  
DB 567 VYAFYFVNKLIDIVEFPLSLLYFGYALMVLSEWLLTGTICFYAAAYNFKRIYAAVKID 625

RESULT 2

US-08-959-004-5  
Sequence 5, Application US/08959004  
Patent No. 6197543

GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
APPLICANT: Corley, Neil C.  
APPLICANT: Lal, Preeti  
APPLICANT: Shah, Purvi  
APPLICANT: Kaser, Matthew  
TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/959,004  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0414 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 663 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: ADRETUT06  
CLONE: 2822412  
US-08-959-004-5  
Query Match 27.3%; Score 843.5; DB 4; Length 663;  
Best Local Similarity 31.2%; Pred. No. 2.4e-74;  
Matches 199; Conservative 120; Mismatches 234; Indels 85; Gaps 16;  
QY 9 LPRTRADAEHHTYQKKEEYVLMNMTVGPVHNQETKYFSLPFCVGSKKSISHYHETLG 68  
DB 41 LAPVNCDEEKKSDCKAEIELFVNRILDSVES-VLPEYVTAQDFCOASEG--KRPSENLG 97  
QY 69 EALQGVLEEFSGLDIKFKDD-----VMPATY-CEILDREKRDFAVYAKHNHYOMYID 122  
DB 98 QVLFGRIEPSPYKFTFNKKETCKLYCTTKTYHTEKAEDQKLEFLKSKMLNLYQHWHVD 157  
QY 123 DLPI-W-----GIVGEADENGED-VYLTW----- 144  
DB 158 NMPVTWCYDVEDQRCNCFPGICGYITDKGHAKDACVSSDFHERDTFYFNHVDIKY 217  
QY 145 YKKLETGFNGNRIV-----DYNLTSEKGVKVLVPTNKTMYSY 180  
DB 218 YHVETGSMGARLVAALKLEPKSPKTHIDKPCSGPMDISNKAAGEI-----KIATY 271  
QY 181 SVKWKSD-VKPEDRFKYLDPSPFOHRIHWFISFNFMVIFLVGLVSMILMRLTKDY 239  
DB 272 SVSFEEDDKIRWASRDYILESMPTH-IQWFSIMNSLVIVLFLSGVAMIMLRLTKDI 330  
QY 240 ARYSKEEEMDDMDRLGDEYGNKQVHGVFRPSSHPILFSSLGSCQIFAVSLIIVIA 299  
DB 331 ARYN---QMDSTE-DAQEEFGWKLHVGDIERPRKGMILSVFLGSGTQILIMTFVLFFA 386  
QY 300 MIEDLY-TERGSMLSIAFYAATSPVNGYFGGSLYAROGGRWIKOMFIGAFLIPAMVC 358  
DB 387 CLGFLSPANRGAALMTCAVVLWLLGTGPAGVAAARFYKSPGEGKKNVLLTSLPCGIVF 446  
QY 359 GTAFFINFAIYHSAIRAIPTGTMAVCCICFVILPLNLVGTILGRNLSGQNPFCRVN 418  
DB 447 ADFFIMNLILWGEESAAIPFGTLVAIALALWFCISVPLTFIGAIFGKKNAIEH-EVRTN 505  
QY 419 AVPRPIKKEWMEPAVIVCLGILPFGSIFTEMFIETSEWAKIYVYVGMVLVIL 478  
DB 506 QIPRQIPEQSFTYKPLPGIIMGILPFGICFQLFLLINSINSHQWYVFGFLVFLFIL 565  
QY 479 CIVTVCTIVCTYFLLNAEDYRWQWTSFLSAASTAIYVYMYSPYFFTKMYGLFQTSF 538  
DB 566 VITCSEATILLCYFHLCAEDYHQQWRSFLTSGTAVYFLIYAVHYFYSKLQITGTASTIL 625  
QY 539 YEGYMAVFTALGICGAIGYMGTSFAVRKIYTNVKID 576  
DB 626 YFGYTMIMVILFLFTGTIGFFACFWEVTKIYSVVKVD 663



RESULT 3  
US-08-959-004-11  
; Sequence 11, Application us/08959004  
; Patent No. 6197543  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Kaser, Matthew  
; TITLE OF INVENTION: HUMAN VESICLE MEMBRANE PROTEIN-LIKE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/959,004  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0414 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 667 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 2131246  
; US-08-959-004-11

Query Match 22.5%; Score 694; DB 4; Length 667;  
Best Local Similarity 27.0%; Pred. No. 1.3e-59;  
Matches 175; Conservative 116; Mismatches 254; Indels 102; Gaps 14;  
QY 21 TYQDKEEVLMNTVGP---YHNROE-----TYKYFSLPFCVGVSKKSIHY 63  
DB 32 TYRENDNIPLLVNHILTPSMYQHKDEGNVSGDKENFLYSYDYNNRHFECQPEKVEQ 91  
QY 64 HETLGEALQGVLEFSGLDIKFKDDVMPATYCEIDLKRDFAFYAIKKNHWYQMYIDD 123  
DB 92 PESLGSVIFGDRINSPFLQNMLOKECESLCKTVIFGDDAKFKNLKNGFFONWLIDG 151  
QY 124 LP-----IWGIVGEADENGEDYIYLT-----YK 146  
DB 152 LPAAREYVDGRKTSFYGAGFNLFQVOTQGTDEATPKGAETTDKQVLETRNDRNMVK 211  
QY 147 KLEIGFNGNR---IVDNLNLTSEGVKLV-----PNT----- 174  
DB 212 TYELPYFANFHDIMIEYHNRGEGNRYVGVIVPEVPSIKRSSPGTCTTGSPLMLDEGNDN 271

QY 175 KIQMSYSVKKKSDVKFEDRPDKYL---DPSEFQHRHWFHSIFNSFMMVIFLVGLVSMIL 231  
DB 272 EVYFTYSVKFENESATSWATRWKYLHVYDPS-----IQWFSLINEFLVVLSSVVIHSL 326  
QY 232 MRTLKDYARYSKKEEMDDMDRLDGEYGWKQVHGDFRPSHPLIFSLIGSGCOIFAV 291  
DB 327 LRAKSDFARYN-ELNLDL---DFQEDSGWKLNHGDFRSPSQSLTSLILVSGGVQLFLM 382  
QY 292 SLIVTIIVAMIEDLY-TERGSMLSTAIFYAATSPVNGYFGGSLYARQGRWIKOMFTGA 350  
DB 383 VTCISFFAALGFLSPSSRGSLATVMFIYALFGFVGSYTSMGIFYKFFNGPYWKANLIITP 442  
QY 351 FLIPAMVCGTAFFINFIAYIYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGNLSGQ 410  
DB 443 LLVPCAILLIILAIUNFFLMFVHSSGVIPASTLFFMVLFWLFESIPLSFAGSLIARKCHW 502  
QY 411 PNFPCRVNAVPRPIPEKKWFMEPAVIVCLGILPGSTFIEMWYFTFSFAYKYVYVGF 470  
DB 503 DEHPTKTNOIARQIPFQPWLYLKTTPATLIAGIFPPFGSIARELYFTYTSLWENKIFYMEGF 562  
QY 471 MMLVLVILCVTCVTIVCTYFLNNAEDYRWQWTSF-LSAASTAIYVYVMSFYFFKTK 529  
DB 563 LFFSELLTLTSSLVTLITLTHSLCLENKWKQWRGFIIGGAGCADIYFIHST--LFTKFK 620  
QY 530 MYGLFQTSFYFYGMVAVFSTALGIMCGAIGYMGTSFAVRKIYTNVKID 576  
DB 621 LGGFTTIVLYGVSYSVISLLCCLVTGSIIGFISMLFVRKIYSSIKVD 667  
RESULT 4  
US-09-134-001C-3703  
; Sequence 3703, Application us/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; PRIOR FILING DATE: 1998-08-13  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3703  
; LENGTH: 496  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
; US-09-134-001C-3703

Query Match 3.8%; Score 118.5; DB 4; Length 496;  
Best Local Similarity 20.0%; Pred. No. 0.0035;  
Matches 81; Conservative 68; Mismatches 156; Indels 99; Gaps 18;  
QY 208 IHWFSEIENSF---MMVIFLVGLVSMILMRTRKDYARYS---KEEEMDDMDRLDGEYGWK 262  
DB 7 MNYLKQYESFPWLIGIFIFLYLIMAILPLSTTDHAYKVNLSQVLTQENGYLGHLEFW 66  
QY 263 QVHGDFRPSHPLIFSLIGSGCOIFAVS--LIVTIIVAMIEDLYTERGSMSTAIFYA 320  
DB 67 AVHNIIIR-----ALIVATTSFLVILVAVMVQLHTRNRYFILLS--FVLM 109  
QY 321 ATSPVNGYFGGSLYARQGRWIKOMFIGAP-LIPAMVCGTAFFINFIATYIYHASRAIPF 379  
DB 110 VTVP-----NTIYSETYG--W-----ETGFPSYIPATV--LSLFILETVVAKWIESHD--- 152  
QY 380 GTWAVAVCCICFFVILPLNLVGTILGNLSGQPNFPCRVNAVPRPIPEKK---WNEPAVI 436  
DB 153 ----TVSEMQLWVFLVSLFGQFFLENLSIANSLIILIGMVYVYFVKKRLSYFLIVGFM 208  
QY 437 VCLGGILPFGSIFTIEMVFIF-----TSFWAYKIYVYVGFN--MLVL 475

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Db 209 SCIGNIIFLNF---NYFLIKDGLNTHYSISDSHGMIHKAGVTLFKLVPEYMFNQMIIL 265
QY 476 VILCIVTV-----CVTI-VCTYFLLNAEDYRQWTSFLSAA- 510
Db 266 TVISIVSIVLLKQNKSLKMRVYIKPLLGLLTPYIKFYVNOQHFELYKASFSIAVL 325
QY 511 -STAIYVYMSFYFFKTKMYGLFQTSFYFGYMAVFSALGIM 553
Db 326 NTTICFYMSIVVYVFKMQORVIRMVMSFIAMASSVLPLL 369

RESULT 5
US-09-134-001C-3057
; Sequence 3057, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: CTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3057
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3057
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Query Match 3.6%; Score 112.5; DB 4; Length 237;
Best Local Similarity 20.7%; Pred. No. 0.0047;
Matches 51; Conservative 45; Mismatches 77; Indels 73; Gaps 12;

QY 352 LIPAMVGTAF-FT-----NFTAIYHASRAIPFGTMVAVCCIFVILPLNLVGTILG 404
Db 3 LLLAYTCSIIFLYQPCNONIKLQVLYSR-----SHCDFCHTIIKPLDLLPIISF 54
QY 405 RNLSGQNPFCRNVAPRPIPEKKWFMEPAVIVCLGILPGSIFIBMYFIFTSFWAYKI 464
Db 55 LKLRGQSR--CCNOPLQR-----LVLIGELVSGAIFL-----YYPT 89
QY 465 YYVYGFNMLVLVICIVTVCTVYVYFLLNAEDYRQWNT-SFLSAASTAIY-----VY 517
Db 90 HFNHETFLTITLFLTMCLYDIHSMHI---DMRLLFYTVVSVFTTQTYGCFNFMIF 145
QY 518 MYSFYFFKTKMYG-----LFQTSFYFGYMAVFSALGIMCGAIGYMGTSAF 565
Db 146 LISHVYLFASKFIGYGDILLFNILGLIFLPLNFFF-FIVVFTFIIG-----GIFAI 195
QY 566 VKRIYT 571
Db 196 ILKIFS 201
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```
RESULT 6
US-08-742-440A-6
; Sequence 6, Application US/08742440A
; Patent No. 5892014
; GENERAL INFORMATION:
; APPLICANT: Coughlin, Shaun
; APPLICANT: Ishihari, Hiroaki
; APPLICANT: Connolly, Andrew
; TITLE OF INVENTION: Protease Activated Receptor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
```

```
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,440A
; FILING DATE: 30-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: UCAL/060PAT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650 327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; US-08-742-440A-6

Query Match 3.5%; Score 107.5; DB 2; Length 408;
Best Local Similarity 18.9%; Pred. No. 0.032;
Matches 56; Conservative 43; Mismatches 122; Indels 75; Gaps 10;

QY 275 PLFSSLLIGSCQIFAVSLIIVIAMIEDLYTERGSMSTAIFAVYAATSPVNGYFGSLY 334
Db 117 PAIYLLVYVGVANAVTLMLLFFRTSICITVYTNLAIADELFCVTLFP-----KIA 170
QY 335 ARGGRRWI-----KOMFGAFLIPAMVCGTAFFINFAIYY-HASRAIPFGTMVA 384
Db 171 YHLNGNWNVEGVLCRATTIVIFYGNMYCSILLACISINRYLAIVHPFTYRGLPKHTYAL 230
QY 385 VCC-----ICFFVLPLNLVGTILGRNLSGQNPFCRNVAPRPIPEKKWFMEPAVIVC- 438
Db 231 VTCGLVNAVTVLYMLPFFI-----LKOEYLVQPDITTC 265
QY 439 -LGGILPFGSIFTEMVFIFTSFWAYKIYYVYGFMM-LVLVILCIVTVCTVICTYFLNLA 496
Db 266 DVINTCESSPFOLYFISLAF-----FGLIPVLIYCYAAIIRT-----LNA 310
QY 497 EYRWQW-----TSFLSAASTAIYVYMSFYFFKTKMYGLFQTSFYFG 541
Db 311 YDHRWLWYVKASLLILVIFTICFAPSNIILIIHHANYNYNTDGLYFIYLIACLG 366

RESULT 7
US-09-576-160B-6
; Sequence 6, Application US/09576160B
; Patent No. 6469150
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; APPLICANT: Zhao, Jiugiao
; APPLICANT: Swanson, Robert
; APPLICANT: Webb, Maria
; APPLICANT: Strohl, Barbara
; TITLE OF INVENTION: Cloning and Characterization of Genes Encoding
; TITLE OF INVENTION: Bradykinin B1 Receptor Homologues From Five Mammalian
; TITLE OF INVENTION: Species
; FILE REFERENCE: 1073.058
; CURRENT APPLICATION NUMBER: US/09/576,160B
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/440,674
; FILING DATE: May 15, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/107,347
; FILING DATE: August 16, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Alan M. Gordon
; REGISTRATION NUMBER: 30637
; REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; FEATURE:
; NAME/KEY: Schizosaccharomyces pombe sts gene
; PUBLICATION INFORMATION:
; AUTHORS: M. Shimanuki, M. Goebel, M. Yanagida,
; AUTHORS: and T.
; AUTHORS: Toda
; TITLE: Fission Yeast sts1+ Gene
; TITLE: Encodes a
; TITLE: Protein Similar to the Chicken Lamin B Receptor
; JOURNAL: Molecu-
; JOURNAL: lar Biology of the Cell
; VOLUME: 3
; PAGES: 263-273
; PAGES: Sequence set out in Figure 1, page 264
; Patent No. 5525496
; DATE: 1992
; RELEVANT RESIDUES IN SEQ ID NO: open reading frame
;
; US-08-440-674-4

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Query Match 3.4%; Score 104.5; DB 1; Length 453;
Best Local Similarity 20.3%; Pred. No. 0.074;
Matches 55; Conservative 46; Mismatches 103; Indels 67; Gaps 13;

QY 361 AFFINIAI-VYHSAIPAIP-----FGTMVAVCCICFFVILPLNLVGTIL-----G 404
Db 121 SFYTTIVILAVLHVTHVPTITTFIDMFGLMSVAITAFVCTFVLVYTGTLFGDRFLDXP 180

QY 405 RNLSGQNPFCRVNAVPRP-----IPEKKWFMEPAV-----IVCLGGIL-----PFGSIFI 450
Db 181 HRLSGNPYDAFMGACLNPRLGKLLDFKMFVEVRIPWFLFTISVGAARQVETVGTVSP 240

QY 451 EMYFIFTSPAY-----KIIYVYGFMMVLVILCVTVIVCVTVIV-CTYEL 493
Db 241 QVLFVCLGHLVYANACSGEQILVITWDMAYEKFGFM-----LIFNMAGVPFTYSHCTIYL 297

QY 494 LNAEDYRWMTSFLSAASTAIYVYVSYFYF-----FKTKMYG--LFTQSFYFYG 542
Db 298 FSHDPSVYVWS---TQYTTGIVILLCCYYIFDTGNGQKNHFNQIYGEVHRKTFPQLP 354

QY 543 MAVFTALGIMCAIGYMGTSA---FVRKIY 570
Db 355 WLIIRKPTFIRCANGTLLTSGWRYARKIH 385

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RESULT 10
PCT-US94-00198-3
; Sequence 3, Application PC/TUS9400198
; GENERAL INFORMATION:
; APPLICANT: Schering Corp.
; TITLE OF INVENTION: RAS Associated GAP Proteins
; NUMBER OF SEQUENCES: 6

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering Corp.
; STREET: 1 Girald Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 6.0.8
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00198
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/004,824
; FILING DATE: 15-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: DX0352 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)822-7255
; TELEFAX: (201)822-7039
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2938 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; PCT-US94-00198-3

Query Match 3.3%; Score 101.5; DB 5; Length 2938;
Best Local Similarity 20.5%; Pred. No. 2.3;
Matches 99; Conservative 78; Mismatches 172; Indels 135; Gaps 26;

QY 132 EADENGEDYLLWTKKLEIGFNGNRIVDNLTSBGKVLKVPNTKIQMSYSVKKVKSVDV-- 189
Db 2466 ERNRKNDIVCTAFARQKLN-----ISGFSQEKGRVLPNFAAS-SFSSKFGTLDLFT 2517

QY 190 -----KFRDFDKYLDPSFFQHRHWFISFNSEFMVIFVLGLVSM----- 229
Db 2518 KNIMLLMEVGSISEGAQWEAKYKYLMDAIFGHR-----SFFSARAMMI--LGIMSKSHTS 2571

QY 230 -----ILMRTLKDYAR-----YSKEEEMDDMDRDLGDEYGNKQVHG 266
Db 2572 LFLCKELLVETM-KVFAEPVVDDEQMFIIAHVFTYSKIVEGLDPSSELMKELFWL---A 2627

QY 267 DVFRSPSHPLIFSSLLGSCQIFAVSLIIVIAMIEDLYTER-----GSMLSTAFIV-- 318
Db 2628 TTCVESPHPLLF-----EGLLLFMVN-----CLKRLTYVHLQLGFGDKSLAKLMESR 2675

QY 319 -YAAT--SPVNGYFGSGSLYARQGRRWIKQMFIFAGFLIP-----AMVCGTAFFINFIAY 370
Db 2676 NEAATLLAKLESY-NGCIWNEDNFPHILGFTIANGLSIPVVKGAALDCLOALFKN---T 2730

QY 371 YHASRAIPGTMVAVCCICFFVILPLNL-----VGTILGRNLGQNPFCRVNAVPRPIPE 426
Db 2731 YVERKSNPKSSDY----LCYLEFLHLVLSPEQLSTLL-LEVGFEDLVPLNNTLVPLTL 2785

QY 427 KKWF---MEPAVIVCLGGILPFGSIFIEYFTFSFWAKIYVYVGFMMVLVILCVIV 483
Db 2786 INWSSDSKSNIVLYQGALLFSCVMSDDPCKFR-----FALLMYLKLKVNPI 2833

QY 484 CVTIVCTYFLLNAEDYRWMTSFLSAASTAIYVYVSYFYFEEKTKMYGLFOTSEYFGYM 543
Db 2834 C---VFRFYTLTRKEER--RLSTLEQSSSEAVAV---SF-----ELIGMLYTHSEFNVL 2878

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QY 544 AVFS 547
Db 2879 EEPN 2882

RESULT 11
US-08-149-100-2
: Sequence 2, Application US/08149100
: Patent No. 5559021
: GENERAL INFORMATION:
: APPLICANT: Smith, Kelli E.
: APPLICANT: Weinshank, Richard L.
: TITLE OF INVENTION: DNA ENCODING A NOVEL MAMMALIAN
: TRANSPORTER HOMOLOGOUS TO NEUROTRANSMITTER TRANSPORTERS
: TITLE OF INVENTION: AND USES THEREOF
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Cooper & Dunham
: STREET: 30 Rockefeller Plaza
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10112
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/149,100
: FILING DATE: 08-NOV-1993
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: White, John P.
: REGISTRATION NUMBER: 28,678
: REFERENCE/DOCKET NUMBER: 44744/JPW/TEP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 977-9550
: TELEFAX: (212) 6640525
: TELEX: 422523 COOP UI
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 616 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-149-100-2

Query Match 3.2%; Score 99.5; DB 1; Length 616;
Best Local Similarity 19.4%; Pred. No. 0.36;
Matches 118; Conservative 80; Mismatches 198; Indels 211; Gaps 35;

QY 90 MPATYCEIDLDKERRAFV-----YAKN--HYWY--Q 118
Db 80 MPLYLELAVGQRMQSGISAWRTISPLSGVGASVVSFFLSMYNINAWGFWYLFH 139
QY 119 MYIDDLPIW-----GIVGADENGEDYLLWTKKLEIGFNGNRIVDVNLTSSEGV 168
Db 140 SFODPLP-WSVCPUNSRGTGYDECEKASQTQYFWYRKTLNI----- 180
QY 169 KLVNPTKIQMSYSVKWKKSVDKPEDRDKYLDPSFFQHRHWFSEIF-----NSPMVVI 221
Db 181 ----SPSIQENGWQW-----EPALCL-TLAWLMVYLCILRGTESTGKV 220
QY 222 FLVLGVS-----MTLMRTLKRDYARYSKEEEMDDMDRLDGEYGVQVHGDFVRPSSHPL 276
Db 221 YFTALMPYCVLIIVLRGLTLHGATGLMYMFTPKIEQLANPKAWINAATQIF--FSLGL 278
QY 277 IFSSLI-----GSCQIFAVSLIIVIAMIEDLYTERGSMLSLTAIFVVAAT----- 322
Db 279 GFGSLIAFASYNFSPNDCQKHAV-----IVSVTNSSTSIIFASIVTFSIYGFKATFNENC 333
QY 323 -----SPVNGYFGGSLYARQGRRW--IKQWFIGAFLIPAM 356

Db 334 LNKVILLTNSFDLEDGFLTASNLEEVKDYL-ASTYPNKYSEVFPHIRNCSESELNTA- 391
QY 357 VCGTAFATFINFATYYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLGQGNPFCR 416
Db 392 VQGTG--LAFT-VYAEATKNNEVSQLSV--LYFFMLLMIGM-GSMLGNTA----- 436
QY 417 VNAVPRPIPEKK---WFMEPAV--IVCLGGILPFGSFTFMYFIPT----SFWAYKIYY 466
Db 437 --AALTPLTDSKVISSYLPKRAISGLVCL-----INCAVGMVFTMEAGNYW-FDIFN 485
QY 467 VYGFMLVLVLCTIVTCVTIYCYFLNLAE-DYR-----WQWTSFJSAASTAIYVY 517
Db 486 DYAAATSLLLIVLVTIAVCV--YGLRRFESDLRAMTGRPLNWKYKAMWAFVSPLLIIG 543
QY 518 MYSFY---YFFFKTKMY-----GLFQTSFY-----FGYMAVFSTALCIMGCAGYM 560
Db 544 LFIFYLSDYILTGTLOYQAWDATQGLVTKDYPPHALAVIGLLVASST---MCIPLVAL 599
QY 561 GTSAFVR 567
Db 600 GT--FIR 604

RESULT 12
US-08-724-394A-10
: Sequence 10, Application US/08724394A
: Patent No. 5872237
: GENERAL INFORMATION:
: APPLICANT: Feder, John N.
: APPLICANT: Kronmal, Gregory S.
: APPLICANT: Lauer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
: TITLE OF INVENTION: Sequences and Antibodies Thereto
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,394A
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitts, Renee A.
: REGISTRATION NUMBER: 35,136
: REFERENCE/DOCKET NUMBER: 017957-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 470 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..470
: OTHER INFORMATION: /note= "NPT3"
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; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; DESCRIPTION: peptide  
US-08-514-451A-7

Query Match 3.1%; Score 95; DB 2; Length 367;  
Best Local Similarity 21.0%; Pred. No. 0.47;  
Matches 75; Conservative 44; Mismatches 122; Indels 116; Gaps 19;

QY 261 WKVHGQDVRPS-----SHPLIF-----SSLIGSCQIFAVSLVII-----VAMIED 303  
Db 10 WEVLHGSHFOGNLSLNETVPHHLLLNASHAFPSGLKVTIVGLIIAIVCIGLLGMLV 69  
QY 304 LYT-ERGSMLSTALFVY-----AATSPVNGY-----FGSLYAROGGRWI 343  
Db 70 MYVILRTPKKKTATNIIFNLALADTLVLTLPQGGDILLGFPGKALCKTVIADYY 129  
QY 344 KQPIGAFILPAMVCGTAFFINFIAIYYHASRAIPFGT-----MVAVCCICFFVILPL 396  
Db 130 K-MFTSTFTLTAMSD-----RVVAI-CHPIRALDVRTSSKAQAVMAIWAASVVGVPV 182  
QY 397 NLVGTILGRNLGQPNPCRVNAVPRPIPEKKWFMPEPAVIVCLGILPFGSIFIEMFYIF 456  
Db 183 -----AIMGSAQVDEETIECLVEI-----PAPQDYW-GPVFAICI-----FLFSFIIPVLII 228  
QY 457 TSFWAYKIYVYVGMPLV-----LVILCIVTVCTIVCTYFELLNAEDYRWOMTS 505  
Db 229 SVCYSLMIRLGRVLLSGRKKDRNLRTRTLRVLVVVAVTVGC-----WT- 274  
QY 506 FLASAASTAIYMYSYFYFFFKTKMYGLFQTSFVFGYMAVFESTALGIM--CGAIGYM 560  
Db 275 -----PVAVEVLVVG-----LGVPQGSSETAVAILRECTALGYV 307

RESULT 15

US-08-313-553-13  
; Sequence 13, Application US/08313553  
; Patent No. 5641650

GENERAL INFORMATION:

APPLICANT: TURNER, George J.  
APPLICANT: BETLACH, Mary C.  
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS POLYPEPTIDES  
TITLE OF INVENTION: IN HALOBACTERIA  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Walter H. Dreger  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/313,553  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/038,662  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Walter H.  
REGISTRATION NUMBER: 24,190  
REFERENCE/DOCKET NUMBER: A-57669/WHI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:

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; LENGTH: 425 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-313-553-13

Query Match 3.1%; Score 94.5; DB 1; Length 425;  
Best Local Similarity 20.4%; Pred. No. 0.65;  
Matches 92; Conservative 75; Mismatches 162; Indels 123; Gaps 23;

QY 168 VKLVNPTKIQMSYVKWKSDVKPFEDFKYLDPSFFQHRHWFHSIFNSFMVIFLVGLV 227  
Db 2 LELLP-TAVEGVSQAQIQALDYKDDDDVDATLDPRSF----- 37  
QY 228 SMILMRTLKDYARYSKEEEMDDMDRLDGLDEYCHKQVH-----GDYFRP 271  
Db 38 ---LLRNPNOKYEPFWEDEKNESGL---TEYRLVSNKSPLOKQLPATISEDASLYLT 91  
QY 272 SSHPLIFSSLIGSCQIFAVSL---IVIIAMIEDLTERGSM-----LSTAIFVYAATS 323  
Db 92 SSWLTLEFVPSVYTG--VFVVSLLPLNINAIIVVFILKMKVKKPAVYMLHLATADLVFVSVL 149  
QY 324 P--VNGVFGSLYARQGRRWIKOMFIGAFILPAMWCGTAFFINFIAIYYHASRAIPFGT 381  
Db 150 PFKISYYFSGDW--QFGSELCL--FVTA-----AFYCNMYA-----SILLMT 188  
QY 382 MVAVCCICFFVILPLNLVGTILGRNLGQPNFPCR-----VNAVPRPIPEKKWFMPEA 434  
Db 189 VISIDRF-LAVVYPMQ---SLSWRTL-GRASFTCLAIWALAIAGVVPVLVLEQTIQVPL 243  
QY 435 VIVCLGGILPFGSIFIEMY--FIFTSEWAYKIYVYVGMPLVILVILCIVTVCTIVCTYF 492  
Db 244 NITTCDDVL--NETLLEGYAYYFSAFSA-----VFFEVPLIISTVCYVSI---IRCLSS 293  
QY 493 LLNAEDYRWOMTSFLSAASTAIYMYM-----YSFYFFFKTKMYGLFQTSFYFG 541  
Db 294 SAVANRSKSRALFLSAAVFCIFICFGPTNVLLIAHYSFLSHTSTTE-----AAYFA 346  
QY 542 YM-AVFESTALGIMCGAIGYMGTSAFVRKIYT 571  
Db 347 YLLCVCVSSISSCIDPLIYYIASSECQRYVYS 378

Search completed: January 20, 2003, 14:28:16  
Job time : 42 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 18, 2003, 20:52:42 ; Search time 40 seconds  
(without alignments)  
1918.809 Million cell updates/sec

Title: US-09-319-724a-14

Perfect score: 3089

Sequence: 1 AALMLLLLLLPRTRADEHEH.....IGYMGTSFAFRKIYTNVKID 576

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3089	100.0	579	21	Human SM-11044-bin
2	3089	100.0	582	21	Human SM-11044-bin
3	2923	94.6	545	22	Human protein sequ
4	2916	94.4	545	21	Human secreted pro
5	2786	90.2	530	22	Human secreted pro
6	2347	76.0	439	19	Non-adrenergic SM
7	2222.5	71.9	567	22	Drosophila melanog
8	2123	68.7	399	22	Human polypeptide,
9	1902	61.6	360	22	Human secreted pro
10	1757	56.9	329	22	Human polypeptide,

11	1757	56.9	329	22	AAB92687	Human protein sequ
12	1710	55.4	589	21	AAG21345	Arabidopsis thalia
13	1710	55.4	608	21	AAG21344	Arabidopsis thalia
14	1669	54.0	583	21	AAG45638	Arabidopsis thalia
15	1669	54.0	602	21	AAG45637	Arabidopsis thalia
16	1668	54.0	589	21	AAG30789	Arabidopsis thalia
17	1558	50.4	537	22	AAB75597	Gene 41 human seq
18	1519.5	49.2	496	21	AAG21346	Arabidopsis thalia
19	1478.5	47.9	430	21	AAG45639	Arabidopsis thalia
20	1477.5	47.8	436	21	AAG30790	Arabidopsis thalia
21	1426.5	46.2	461	21	AAG30791	Arabidopsis thalia
22	1448.5	37.2	592	21	AAG36371	Arabidopsis thalia
23	1446.5	37.1	592	21	AAG32077	Arabidopsis thalia
24	950.5	30.8	642	21	AA80519	Human putative SST
25	950.5	30.8	642	23	AAU74740	Human Phgl protein
26	944	30.6	607	21	AAB38332	Human secreted pro
27	943.5	30.5	467	21	AAG36372	Arabidopsis thalia
28	938.5	30.4	467	21	AAG32078	Arabidopsis thalia
29	936.5	30.3	630	22	ABB63203	Drosophila melanog
30	898	29.1	609	21	AAG31959	Arabidopsis thalia
31	898	29.1	624	21	AAG31958	Arabidopsis thalia
32	898	29.1	659	21	AAG31957	Arabidopsis thalia
33	878	28.4	619	21	AAG43743	Arabidopsis thalia
34	860	27.8	641	23	AAU74739	Dictyostelium Phgl
35	859.5	27.8	416	21	AAG36373	Arabidopsis thalia
36	846.5	27.4	416	21	AAG32079	Arabidopsis thalia
37	843.5	27.3	663	20	AAV17390	Human vesicle memb
38	838	27.1	659	22	ABB58205	Drosophila melanog
39	812	26.3	218	23	ABB90443	Human polypeptide
40	810	26.2	517	21	AAG43745	Arabidopsis thalia
41	809	26.2	522	21	AAG43744	Arabidopsis thalia
42	789	25.5	509	21	AAG04118	Arabidopsis thalia
43	747	24.2	370	21	AAG04119	Arabidopsis thalia
44	715	23.1	152	22	AA933268	Human polypeptide,
45	700	22.7	356	21	AAG04120	Arabidopsis thalia

#### ALIGNMENTS

RESULT 1  
AAY82460  
ID AAY82460 standard; Protein; 579 AA.  
XX  
AC AAY82460;  
XX  
XX  
DT 30-JUN-2000 (first entry)  
XX  
DE Human SM-11044-binding receptor protein SEQ ID NO:4.  
XX  
DE Human: SM-11044-binding receptor protein; SMAP; antiasthmatic;  
KW antiinflammatory; inflammation; eosinophil infiltration; asthma;  
KW Intestinal disease; eosinophil migration inhibitor; intestinal stress.  
XX  
XX Homo sapiens.  
XX OS  
XX PN WO200014266-A1.  
XX  
PD 16-MAR-2000.  
XX  
PF 06-SEP-1999; 99WO-JP04808.  
XX  
PR 08-SEP-1998; 98JP-0253771.  
XX  
XX (SUMU ) SUMITOMO PHARM CO LTD.  
XX  
XX Sugawara T, Hidaka J, Kawakami H;  
XX  
XX WPI: 2000-257008/22.  
XX N-PSDB; AAA08361.  
XX  
XX Recombinant human SM-11044-binding receptor protein with ligand binding  
PT activity, useful for developing drugs for inflammation accompanying

PT eosinophil infiltration, asthma and intestinal diseases -  
XX  
PS Example 3; Page 36-39; 41pp; Japanese.

The present invention describes transformed cells which express a recombinant human SM-11044-binding receptor protein (SMBP) at such a high level as to enable the assay of the ligand-binding activity by deleting the polythymidine sequence from the base sequence of the 3'-nontranslation region or the cell membrane fraction. Also described is a method for screening a human SMBP agonist/antagonist characterised by using the transformed cells, cell membrane fraction of the recombinant human SMBP. The recombinant protein is useful for developing drugs for treating inflammation accompanying eosinophil infiltration, asthma, and diseases of intestine, particularly agonists as eosinophil migration inhibitors or relaxing agents for intestinal stress. The protein is easily expressed by transformed cells after deleting polythymidine sequence from base sequence of 3'-nontranslation region. The present sequence represents human SMBP from the present invention.

Query Match	100.0%	Score 3089;	DB 21;	Length 579;
Best Local Similarity	100.0%	Pred. No. 1.9e-301;		
Matches 576;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

Qy	1	AAUWLLLLLPRTRADDEHHTYQDKSEVVLWNTVGPYHNROETKYKFSLPFCVGSKKSI	60
Db	4	AAUWLLLLLPRTRADDEHHTYQDKSEVVLWNTVGPYHNROETKYKFSLPFCVGSKKSI	63
Qy	61	SHYHETLGEALQGVLEFSGLDIKFKDDVMPATYCEIDLDEKRAAFVYAIKNHWYQMY	120
Db	64	SHYHETLGEALQGVLEFSGLDIKFKDDVMPATYCEIDLDEKRAAFVYAIKNHWYQMY	123
Qy	121	IDDLPTWIVGEADENGEDYIYLTWYKKLEIGFNGNRIVDVNLTSBGKVKLVPTNKIQMSY	180
Db	124	IDDLPTWIVGEADENGEDYIYLTWYKKLEIGFNGNRIVDVNLTSBGKVKLVPTNKIQMSY	183
Qy	181	SVKWKSDVKFEDRFQKYLDPSFFQHRIHWFSIFNSFMVIFLVGLVSMILMRTLKDYA	240
Db	184	SVKWKSDVKFEDRFQKYLDPSFFQHRIHWFSIFNSFMVIFLVGLVSMILMRTLKDYA	243
Qy	241	RYSKEEEMDDMDRLGDEYGNQVHGCVPRPSSHPLIFSSLIGSGCOIFAVSLIIVIAM	300
Db	244	RYSKEEEMDDMDRLGDEYGNQVHGCVPRPSSHPLIFSSLIGSGCOIFAVSLIIVIAM	303
Qy	301	IEDLYTERGSMLSIAIFYVAATSPVNGYEGGSLYARQGGRRWIKQMTGAFLIPAMVCGT	360
Db	304	IEDLYTERGSMLSIAIFYVAATSPVNGYEGGSLYARQGGRRWIKQMTGAFLIPAMVCGT	363
Qy	361	AFPIFIYIYHASRAIPGTMVAVCCICFFVLPLNLVGTTLGNLSQGNFPCRVNAV	420
Db	364	AFPIFIYIYHASRAIPGTMVAVCCICFFVLPLNLVGTTLGNLSQGNFPCRVNAV	423
Qy	421	PRPIPEKKWFMFPAVICVLGGILPFGSIFIEMYFIFTSEWAYKIYVYGFMMMLVLILCI	480
Db	424	PRPIPEKKWFMFPAVICVLGGILPFGSIFIEMYFIFTSEWAYKIYVYGFMMMLVLILCI	483
Qy	481	VTVCVTIVCTYFLLNADRYRWQWTSFLSAASAIYVYMYSFYYFEKTKMYGLFQTSYFF	540
Db	484	VTVCVTIVCTYFLLNADRYRWQWTSFLSAASAIYVYMYSFYYFEKTKMYGLFQTSYFF	543
Qy	541	GYMAVFSTALGIMCGAIGYMGTSFAVRKIYTNVKID	576
Db	544	GYMAVFSTALGIMCGAIGYMGTSFAVRKIYTNVKID	579
RESULT 2			
AAV82459			
ID	AAV82459 standard; Protein; 582 AA.		
XX	AAV82459:		
XX	AC		
XX	DT 30-JUN-2000 (first entry)		

RESULT 2  
 AAY82459  
 ID AAY82459 standard; Protein; 582 AA  
 XX  
 AC AAY82459;  
 AC

XX	Human SM-11044-binding receptor protein SEQ ID NO:2.
XX	
XX	
XX	Human: SM-11044-binding receptor protein; SMBP: antiasthmatic;
KW	antiinflammatory; inflammation; eosinophil infiltration; asthma;
KW	intestinal disease; eosinophil migration inhibitor; intestinal stress.
KW	
XX	
XX	Homo sapiens.
OS	
XX	WO200014266-A1.
PN	
XX	16-MAR-2000.
PD	
XX	06-SEP-1999; 99WO-JP04808.
XX	
XX	08-SEP-1998; 98JP-0253771.
PR	
XX	(SUMU ) SUMITOMO PHARM CO LTD.
XX	
XX	Sugasawa T, Hidaka J, Kawakami H;
PI	
XX	WPI: 2000-257008/22.
XX	N-PSDB; AAR08360.
DR	
XX	Recombinant human SM-11044-binding receptor protein with ligand binding
PT	activity, useful for developing drugs for inflammation accompanying
PT	eosinophil infiltration, asthma and intestinal diseases -
PT	
XX	Example 1; Page 29-32; 41pp; Japanese.
PS	
XX	
XX	The present invention describes transformed cells which express a
CC	recombinant human SM-11044-binding receptor protein (SMBP) at such
CC	a high level as to enable the assay of the ligand-binding activity by
CC	deleting the polythymidine sequence from the base sequence of the
CC	3'-nontranslation region or the cell membrane fraction. Also described
CC	is a method for screening a human SMBP agonist/antagonist characterised
CC	by using the transformed cells, cell membrane fraction of the
CC	recombinant human SMBP. The recombinant protein is useful for developing
CC	drugs for treating inflammation accompanying eosinophil infiltration,
CC	asthma, and diseases of intestine, particularly agonists as eosinophil
CC	migration inhibitors or relaxing agents for intestinal stress. The
CC	protein is easily expressed by transformed cells after deleting
CC	polythymidine sequence from base sequence of 3'-nontranslation region.
CC	The present sequence represents human SMBP from the present invention.
CC	
XX	
XX	Sequence 582 AA:
SO	

Query Match	100.0%;	Score 3089;	DB 21;	Length 582;
Best Local Similarity	100.0%;	Pred. No. 1.9e-301;		
Matches 576;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	AALWLLLLLPRTRADHEHTYQDKEEVWLMMNTVGPYHNRQETKYKFLSPFCVGSKSI	60	
Db	7	AALWLLLLLPRTRADHEHTYQDKEEVWLMMNTVGPYHNRQETKYKFLSPFCVGSKSI	66	
QY	61	SHYHETLGEALQGVLEFSGLDIKFKDDVMPATYCEIDLDKEKRDADFVIAIKNHWTQMY	120	
Db	67	SHYHETLGEALQGVLEFSGLDIKFKDDVMPATYCEIDLDKEKRDADFVIAIKNHWTQMY	126	
QY	121	IDPLPWIVGEADENGEDYYLWTYKKLETGFNGNRIVDNLVTSEGVKVLVPNTKIOMSY	180	
Db	127	IDPLPWIVGEADENGEDYYLWTYKKLETGFNGNRIVDNLVTSEGVKVLVPNTKIOMSY	186	
QY	181	SVKWKSDVKFEDRFDKYLDPSFFQRIHWFSPFNPMVIFLVGLVSMILMLRLRKDYA	240	
Db	187	SVKWKSDVKFEDRFDKYLDPSFFQRIHWFSPFNPMVIFLVGLVSMILMLRLRKDYA	246	
QY	241	RYSKEEMDDMDRLDGEYQVHGDKVFRPSSHPLIFSSLGSCCQIFAVSLIIVIAM	300	
Db	247	RYSKEEMDDMDRLDGEYQVHGDKVFRPSSHPLIFSSLGSCCQIFAVSLIIVIAM	306	
QY	301	IEDLYTERGSMLSIAIFVYAATSPVNGYFGSGLYARQGGRRWTKOMFTGAFLIPAMVCGT	360	

[illegible]

Db 307 IEDLYTERGSMSTAIIFYAANTSPVNGYFGGSLYARQGGRRWIKQMFIGAFLIPAMVCGT 366

QY 361 AFFINFIAIYYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLSCGNPFCRVNAV 420

Db 367 AFFINFIAIYYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLSCGNPFCRVNAV 426

QY 421 PRPIPEKKMFMEPAVIVCLGGILPFGSIFTEMFIPTSFWAYKIYYVYGFMMILVLTLCI 480

Db 427 PRPIPEKKMFMEPAVIVCLGGILPFGSIFTEMFIPTSFWAYKIYYVYGFMMILVLTLCI 486

QY 481 VTVCVTIVCTYFLLNAEDYRWQNTSFLSAASTAIYVMTYSFYFFPKTKMYGLFQTSFYF 540

Db 487 VTVCVTIVCTYFLLNAEDYRWQNTSFLSAASTAIYVMTYSFYFFPKTKMYGLFQTSFYF 546

QY 541 GYMAVFSTALGIMCGAIGYMGTSFAVRKIYTNVKID 576

Db 547 GYMAVFSTALGIMCGAIGYMGTSFAVRKIYTNVKID 582

RESULT 3

ID AAB94667 standard; Protein; 545 AA.

XX AAB94667;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:15600.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

PF

PR 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs -

XX

PS Claim 8; SEQ ID 15600; 2537pp + CD ROM; English.

XX

CC The present invention describes primer sets for synthesizing 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by;

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification;

CC of the present invention.

XX

QY Sequence 545 AA;

Query Match 94.6%; Score 2923; DB 22; Length 545;

Best Local Similarity 100.0%; Pred. No. 8.5e-285;

Matches 545; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 MNTVGPYHNRQETKYKFSLPFCVSGSKKSHYHETLGEALOGVELEFSGLDIKFKDDVMP 91

Db 1 MNTVGPYHNRQETKYKFSLPFCVSGSKKSHYHETLGEALOGVELEFSGLDIKFKDDVMP 60

QY 92 ATYCEIDLQEKRDFAFYAIKNHYWYQMYIDDLPIWGIWGEADENGEDYYLWTKKLEIG 151

Db 61 ATYCEIDLQEKRDFAFYAIKNHYWYQMYIDDLPIWGIWGEADENGEDYYLWTKKLEIG 120

QY 152 FNGNRIVDNLTSSEGVKVLVNTKIQMSYSVKWKSDVKFEDRFDKYLDPSPFQHRHWF 211

Db 121 FNGNRIVDNLTSSEGVKVLVNTKIQMSYSVKWKSDVKFEDRFDKYLDPSPFQHRHWF 180

QY 212 SFNSPMWVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLDGEYQWKGVDVFRP 271

Db 181 SFNSPMWVIFLVGLVSMILMRTLKDYARYSKEEEMDDMDRLDGEYQWKGVDVFRP 240

QY 272 SSHPLIFSSLLIGSCQIFAVSLVLIIVAMIEDLYTERGSMSTAIIFYAANTSPVNGYFGG 331

Db 241 SSHPLIFSSLLIGSCQIFAVSLVLIIVAMIEDLYTERGSMSTAIIFYAANTSPVNGYFGG 300

QY 332 SLYARQGGRRWIKQMFIGAFLIPAMVCGTAFINFIATYIYHASRAIPFGTMVAVCCICFF 391

Db 301 SLYARQGGRRWIKQMFIGAFLIPAMVCGTAFINFIATYIYHASRAIPFGTMVAVCCICFF 360

QY 392 VILPLNLVGTILGRNLSCGNPFCRVNAVPRPIPEKKMFMEPAVIVCLGGILPFGSIFTE 451

Db 361 VILPLNLVGTILGRNLSCGNPFCRVNAVPRPIPEKKMFMEPAVIVCLGGILPFGSIFTE 420

QY 452 MYFIFTSFWAYKIYYVYGFMMILVLTLCITVCTVTCVTFLLNAEDYRWQNTSFLSAAS 511

Db 421 MYFIFTSFWAYKIYYVYGFMMILVLTLCITVCTVTCVTFLLNAEDYRWQNTSFLSAAS 480

QY 512 TAIYVYMYSFYFFYFKTKMYGLFQTSFYFGYMAVFSTALGIMCGAIGYMGTSFAVRKIY 571

Db 481 TAIYVYMYSFYFFYFKTKMYGLFQTSFYFGYMAVFSTALGIMCGAIGYMGTSFAVRKIY 540

QY 572 NVKID 576

Db 541 NVKID 545

RESULT 4

ID AAY94910 standard; Protein; 545 AA.

XX AAY94910;

DT 16-JUN-2000 (first entry)

XX

DE Human secreted protein clone pk366\_7 protein sequence SEQ ID NO:26.

XX

KW Human; secreted protein; immunestimulant; immunosuppressant; virucide;

KW antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;

KW antidiabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;

KW antithyroid; immune deficiency; severe combined immunodeficiency; SCID;

KW infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;

KW connective tissue disease; multiple sclerosis; erythematosis;

KW rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;

KW Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;  
KW insulin dependent diabetes mellitus; graft-versus-host-disease;  
KW autoimmune inflammatory eye disease; allergy.  
OS Homo sapiens.  
XX WO200009552-A1.  
PN PD 24-FEB-2000.  
XX PF 13-AUG-1999; 99WO-US18298.  
XX PR 14-AUG-1998; 98US-0096622.  
PR 17-AUG-1998; 98US-0096815.  
PR 04-SEP-1998; 98US-0099229.  
PR 23-OCT-1998; 98US-0105368.  
PR 08-JAN-1999; 99US-0115234.  
PR 12-FEB-1999; 99US-0119931.  
PR 18-FEB-1999; 99US-0120575.  
PR 30-APR-1999; 99US-0132020.  
PR 11-AUG-1999; 99US-0096622.  
XX (GEMY ) GENETICS INST INC.  
PA Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ, Spaulding V;  
PI Wong GG, Clark HF, Fechtel K;  
XX WPI: 2000-205979/18.  
XX New polynucleotides encoding secreted proteins, which may have e.g.  
PT nutritional, chemokine, immune stimulating or suppressing,  
PT hematopoiesis regulating, tissue growth, activin/inhibin  
PT antiinflammatory or tumor inhibition activity  
XX Claim 35; Page 494-495; 641pp; English.  
XX AAA16618 to AAA16697 encode the human secreted proteins given in  
CC AAY94898 to AAY94980, isolated from human adult brain, adult thyroid,  
CC adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,  
CC adult placenta, adult testis, whole embryo, adult cartilage, kidney,  
CC foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,  
CC and adult bladder, cDNA libraries. The polynucleotides and proteins are  
CC predicted to have biological activities which would make them suitable  
CC for treating, preventing or ameliorating medical conditions in humans  
CC and animals. The polynucleotides can be used as markers for tissues in  
CC which the protein is preferentially expressed, as molecular weight  
CC markers on Southern gels, and as chromosome markers or tags to identify  
CC chromosomes or to map gene positions. The proteins can be used in the  
CC treatment of immune deficiencies and disorders, such as severe combined  
CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other  
CC infections. These infections include human immunodeficiency virus (HIV),  
CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and  
CC candidiasis. The proteins can be used to treat autoimmune disorders such  
CC as connective tissue disease, multiple sclerosis, systemic lupus  
CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,  
CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent  
CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and  
CC autoimmune inflammatory eye disease. The proteins can also be used to  
CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent  
CC probes for the human secreted proteins from the present invention.  
XX Sequence 545 AA:  
Query Match 94.4%; Score 2916; DB 21; Length 545;  
Best Local Similarity 99.8%; Pred. No. 4.3e-284;  
Matches 544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 32 MNTVGPYHNRQETKYFSLPCVCGSKSISHYHETLGEALOGVELEFSGLDIKFKDDVWP 91  
DB 1 MNTVGPYHNRQETKYFSLPCVCGSKSISHYHETLGEALOGVELEFSGLDIKFKDDVWP 60  
QY 92 ATYCEIDLKDKRDFAFVAIKNHVYQMYIDDLPIWIGVGEADENGEDYLLWTYKKLEIG 151

Db 61 ATYCEIDLKDKRDFAFVAIKNHVYQMYIDDLPIWIGVGEADENGEDYLLWTYKKLEIG 120  
QY 152 ENGRIVDVNLTSSEGVKLVNPTKIQMSYSVKWKSKDKFEDRFDKYLDPSFFQRIHWF 211  
Db 121 FNGNRIVDVNLTSSEGVKLVNPTKIQMSYSVKWKSKDKFEDRFDKYLDPSFFQRIHWF 180  
QY 212 STFNFSMMVIFLVGLVSMILMRTLRKDYARYSKEREMDDMDRLDGLDEYGWQVHGDVFRP 271  
Db 181 STFNFSMMVIFLVGLVSMILMRTLRKDYARYSKEREMDDMDRLDGLDEYGWQVHGDVFRP 240  
QY 272 SSHPLIFSSLGSGCOIFAVSLIIVIIAMIEDLYTERGSMILSTAFIVYAATSPVNGYFEG 331  
Db 241 SSHPLIFSSLGSGCOIFAVSLIIVIIAMIEDLYTERGSMILSTAFIVYAATSPVNGYFEG 300  
QY 332 SLIYARQGGRRWIKOMFIFAGFLIPAMVCGTAFEFINIAIYYHASRAIPFGTMMVAVCCICFF 391  
Db 301 SLIYARQGGRRWIKOMFIFAGFLIPAMVCGTAFEFINIAIYYHASRAIPFGTMMVAVCCICFF 360  
QY 392 VILPLNLVGTILGRNLGQPNFPCRVNAVPRPIPEKKWFMPEPAVIVCLGGILPFGSIFIE 451  
Db 361 VILPLNLVGTILGRNLGQPNFPCRVNAVPRPIPEKKWFMPEPAVIVCLGGILPFGSIFIE 420  
QY 452 MYFIPTSWAKYIYVYGFMMVLVLICIVTVCVTVICTYFLLNADYRWQNTSFLSAAS 511  
Db 421 MYFIPTSWAKYIYVYGFMMVLVLICIVTVCVTVICTYFLLNADYRWQNTSFLSAAS 480  
QY 512 TAIYVYMYSFYFFPKTKMYGLFQTSFYFGYMAVFEALGMCAGYMGTSAFVRKIYT 571  
Db 481 TAIYVYMYSFYFFPKTKMYGLFQTSFYFGYMAVFEALGMCAGYMGTSAFVRKIYT 540  
QY 572 NVKID 576  
Db 541 NVKID 545  
RESULT 5  
ID AAB75598 standard; Protein; 530 AA.  
XX AAB75598;  
AC AAB75598;  
XX 06-APR-2001 (first entry)  
XX Human secreted protein sequence encoded by gene 41 SEQ ID NO:152.  
KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;  
KW neutropic; neuroprotective; antibacterial; virucide; fungicide;  
KW ophthalmological; vulnary; autoimmune disease; cardiovascular disorder;  
KW hyperproliferative disorders; cerebrovascular disorder; wound healing;  
KW nervous system disorder; ocular disorder; skin ageing; chemotaxis;  
KW food additive.  
XX Homo sapiens.  
OS WO200077026-A1.  
PN PD 21-DEC-2000.  
XX 01-JUN-2000; 2000WO-US14973.  
PR 11-JUN-1999; 99US-0138630.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX Rosen CA, Ruben SM, Komatsoulis GA;  
XX WPI: 2001-071258/08.  
XX N-PSDB; AAF64216.  
XX Nucleic acid molecules encoding human secreted proteins, used in



QY 419 AVPRPIPEKKWMEPAVIVCLGILPFGSIFIDMYFIPTFSWAYKIYYVYGFMMVLVL 478  
 DB 301 AVPRPIPEKKWMEPAVIVCLGILPFGSIFIDMYFIPTFSWAYKIYYVYGFMMVLVL 360  
 QY 479 CIVTVCTIVCTYFLNAEDYRNQWTSFLSAASTAIYVYMYSFYFFKTKMYGLQTSF 538  
 DB 361 CIVTVCTIVCTYFLNAEDYRNQWTSFLSAASTAIYVYMYSFYFFKTKMYGLQTSF 420  
 QY 539 YFGYMAVESTALGIMGAI 557  
 DB 421 YFGYMAVESTALGIMGAI 439  
 RESULT 7  
 ID ABB65162 standard; Protein; 567 AA.  
 XX ABB65162;  
 AC ABB65162;  
 DT 26-MAR-2002 (first entry)  
 DE Drosophila melanogaster polypeptide SEQ ID NO 22278.  
 XX Drosophila; developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 KW Drosophila melanogaster.  
 OS  
 XX WO200171042-A2.  
 PN 23-MAR-2001; 2001WO-US09231.  
 PD 27-SEP-2001.  
 XX 23-MAR-2001; 2001WO-US09231.  
 XX 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX (PEKE ) PE CORP NV.  
 PA Venter JC, Adams M, Li PWD, Myers EW;  
 PI WPI; 2001-656860/75.  
 DR N-PSDB; ABL09265.  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX Disclosure; SEQ ID NO 22278; 21pp + Sequence Listing; English.  
 PS The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (AB857737-AB872072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 567 AA;  
 Query Match 71.9%; Score 2222.5; DB 22; Length 567;  
 Best Local Similarity 70.1%; Pred. No. 2.4e-214;  
 Matches 406; Conservative 64; Mismatches 80; Indels 29; Gaps 2;  
 QY 2 AEWLLLL---LPRTRADEHEITYODKEEVLMWMTVGPYHNQETKYFSLPFCVGSK 57  
 DB 14 ATCLCLLIASCYVLSQADEHNKYNDRREVLMWMTVGPYHNQETKYFSLPFCVGSK 73

QY 58 KSISHVHETLGEALQGVLEFSGLDITKFDKDDVMPATYCEIDLDKRRDAFVAIAKNHYWY 117  
 DB 74 SSISHVHETLSEALQGVLEFSGYEMEFKSDAPKSCIMVTLQEESEAKATYAVKNEYWY 133  
 QY 118 QMYIDDLPLWIGVGEADENGEDYLLATYKLEIGFNGNRIVDNLVNSEGVKLVNPNTKIQ 177  
 DB 134 QMYIDGLPLWIGVGERDERDGKYYIFTHKKFDIGYNGQQIVDITLTEGREELKPGSHIN 193  
 QY 178 MSYSVKKWKSVDKFDKYLDPSPFFQHRHWFSEFNSFMVIFLVGLVSMILMTLTK 237  
 DB 194 FSYEVNWKPSKVEFKNRFDKYLDPNFEFQHRHWFSEFNSFMVIFLVGLVSMILMTLTK 253  
 QY 238 DYARYSKEEEMDDMDRLDGLDEYGWKQVHGDVFRSPSSHLIFSSLGSGCQIFAVSLIVII 297  
 DB 254 DYARYSKEEIDDDMDRLDGLDEYGWKQVHGDVFRSPNTLLFSALVGAGYQLISVWFCVIM 313  
 QY 298 VAMIEDLYTERGSMSTAIYVYAAATSPVANGYFGSGLYARQGGRRWIKOMFIGNFLIPAMV 357  
 DB 314 FAIVGELYTERGSMSTAIYVYAAATSPINGYFGSGLYARLGGRRWIRQLVSAFTYVPAV 373  
 QY 358 CGTAFPIFIATYIYHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLGQPNPCRV 417  
 DB 374 CGTAFILFIATYIYHASRAIPFGTMVAVTCICLVILPLTLVGTV----- 418  
 QY 418 NAVPRPIPEKKWMEPAVIVCLGILPFGSIFIDMYFIPTFSWAYKIYYVYGFMMVLVLVI 477  
 DB 419 -----KWMEPLIIVLLGGVLPFGSIFIDMYFIPTFSWAYKIYYVYGFMMVLVFSI 468  
 QY 478 LCIVTVCTIVCTYFLNAEDYRNQWTSFLSAASTAIYVYMYSFYFFKTKMYGLQTSF 537  
 DB 469 LTVTVCTIVCTYFLNAEDYRNQWTSFLSAAGSTSIYVYAYSFYFFKTKMFLQFQA 528  
 QY 538 FYFGYMAVESTALGIMGAGIYMGTSFAVRYKTYTNVKID 576  
 DB 529 FYFGYMAVESTALGIMGAGIICGTGVGVGTNLVFRKIYSNVKID 567  
 RESULT 8  
 ID AAM93355 standard; Protein; 399 AA.  
 XX AAM93355;  
 AC AAM93355;  
 DT 06-NOV-2001 (first entry)  
 DE Human polypeptide, SEQ ID NO: 2909.  
 XX Human; full length cDNA; cDNA synthesis; oligo-capping.  
 KW Homo sapiens.  
 OS  
 XX EP1130094-A2.  
 PN 05-SEP-2001.  
 PD 07-JUL-2000; 2000EP-0114089.  
 PF 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX (HELI-) HELIX RES INST.  
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 DR N-PSDB; AAK94275.  
 XX 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX Claim 8; SEQ ID NO 2909; 1380pp + sequence listing; English.  
 PS



Db 301 MYSFYFFFKTKMYGLFQTSFYFGYMAVFSTALGIMCGAIGMGTSFAFVRKIYTNVKID 359

AA93524

RESULT 10

ID AA93524 standard; Protein: 329 AA.

XX

AC AA93524;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human polypeptide, SEQ ID NO: 3257.

XX

KW Human; full length cDNA; cDNA synthesis; oligo-capping.

XX

OS Homo sapiens.

XX

PN EP1130094-A2.

XX

PD 05-SRP-2001.

XX

PF 07-JUL-2000; 2000EP-0114089.

XX

PR 08-JUL-1999; 99JP-0194486.

PR

PR 11-JAN-2000; 2000JP-0118774.

XX

PR 02-MAY-2000; 2000JP-0183765.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX

DR WPI: 2001-524255/58.

DR

DR N-PSDB; AAK94454.

XX

PT 830 Primers useful for synthesizing full length cDNA clones and their

PT use in genetic manipulation

XX

PS Claim 8; SEQ ID NO 3257; 1380pp + sequence listing; English.

XX

CC The invention relates to primers for synthesizing full length cDNA

CC clones. 830 cDNA molecules encoding a human protein have been

CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA

CC molecules have been determined. Primers for synthesizing the full length

CC cDNA are useful for clarifying the function of the protein encoded by

CC the cDNA. The full length clones were obtained by construction of full

CC length enriched cDNA libraries that were synthesised by the oligo-capping

CC method. The primers enable the production of the full length cDNA easily

CC without any special methods. The present sequence is a polypeptide

CC encoded by a full length human cDNA of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in CD-ROM format directly from EP0.

XX

SQ Sequence 329 AA:

Query Match 56.9%; Score 1757; DB 22; Length 329;

Best Local Similarity 100.0%; Pred. No. 7.1e-168;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 MDDMDRLDGEYKQVHGQVDFRPSHPHLSFSLGSGQIFAVSLIVIVAMIEDLYTE 307

Db 1 MDDMDRLDGEYKQVHGQVDFRPSHPHLSFSLGSGQIFAVSLIVIVAMIEDLYTE 60

QY 308 RGSMLSTAFVYAATSPVNGYFGSLYARQGGRRWIKQMFIGAFLIPAMVCGTAFFINFI 367

Db 61 RGSMLSTAFVYAATSPVNGYFGSLYARQGGRRWIKQMFIGAFLIPAMVCGTAFFINFI 120

QY 368 AIYTHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLGSGQPNFPCRVNAVPRPIPEK 427

Db 121 AIYTHASRAIPFGTMVAVCCICFFVILPLNLVGTILGRNLGSGQPNFPCRVNAVPRPIPEK 180

QY 428 KWFMEPAVIVCLGILPFGSIFTEYFWAYKIYYVYGFMMVLVLICITVTCVTI 487

Db 181 KWFMEPAVIVCLGILPFGSIFTEYFWAYKIYYVYGFMMVLVLICITVTCVTI 240

QY 488 VCTYFLLNAEDYRWQWTSFLSAASTAIYYVMYSFYFFFKTKMYGLFQTSFYFGYMAVFS 547

Db 241 VCTYFLLNAEDYRWQWTSFLSAASTAIYYVMYSFYFFFKTKMYGLFQTSFYFGYMAVFS 300

QY 548 TALGIMCGAIGMGTSFAFVRKIYTNVKID 576

Db 301 TALGIMCGAIGMGTSFAFVRKIYTNVKID 329

RESULT 11

AA92687

ID AAB92687 standard; Protein: 329 AA.

XX

AC AAB92687;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:11071.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR

PR 27-AUG-1999; 99JP-0300253.

PR

PR 11-JAN-2000; 2000JP-0118776.

PR

PR 02-MAY-2000; 2000JP-0183767.

PR

PR 09-JUN-2000; 2000JP-0241899.

XX

PA (HELI-) HELIX RES INST.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI: 2001-318749/34.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602

PT full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the

PT full-length cDNAs

XX

PS Claim 8; SEQ ID 11071; 2537pp + CD ROM; English.

XX

CC The present invention describes primer sets for synthesising 5602

CC full-length cDNAs defined in the specification. Where a primer set

CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of

CC the 5602 nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in

CC the specification. The primer sets can be used in antisense therapy and

CC in gene therapy. The primers are useful for synthesising polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to

CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632

CC represent oligonucleotides, all of which are used in the exemplification

CC of the present invention.



XX	Seq	Sequence	329 AA;
XX	Query Match	56.9%; Score 1757; DB 22; Length 329;	
XX	Best Local Similarity	100.0%; Pred. No. 7.le-168;	
XX	Matches 329; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	248	MDDMRDLGDEYGWKQVHGDFRPSHPLIFSSLLIGSGCQIPAVSLIIVIAMIEDLXTE	307
Db	1	MDDMRDLGDEYGWKQVHGDFRPSHPLIFSSLLIGSGCQIPAVSLIIVIAMIEDLXTE	60
Qy	308	RGSMLSTAIFYVAATSPVNGFVGGLSYARQGRRWIKOMFIGAFLIPAMVCCTAFFINFI	367
Db	61	RGSMLSTAIFYVAATSPVNGFVGGLSYARQGRRWIKOMFIGAFLIPAMVCCTAFFINFI	120
Qy	368	AIIYHASRAIPFGTMVAVCCICFFVILPLNLVTGLIRNLSQPFPFCRVNAVPRPIPEK	427
Db	121	AIIYHASRAIPFGTMVAVCCICFFVILPLNLVTGLIRNLSQPFPFCRVNAVPRPIPEK	180
Qy	428	KWFMEPAVIVCLGGILPFGSIFIEMVFITFSFWAYKIYYVGFMMVLVLILCIIVTCVTI	487
Db	181	KWFMEPAVIVCLGGILPFGSIFIEMVFITFSFWAYKIYYVGFMMVLVLILCIIVTCVTI	240
Qy	488	VCTYFLLNAEDYRWQWTSFLSAATAIYVVMYSFYIYFEFKMKYGLFQTSFYFGYMVAFS	547
Db	241	VCTYFLLNAEDYRWQWTSFLSAATAIYVVMYSFYIYFEFKMKYGLFQTSFYFGYMVAFS	300
Qy	548	TALGIMCAIGMGTSAFVRKIYTNNKID 576	
Db	301	TALGIMCAIGMGTSAFVRKIYTNNKID 329	
RESULT 12			
AAG21345			
ID	AAG21345 standard; Protein; 589 AA.		
AC	AAG21345;		
DT	17-OCT-2000 (first entry)		
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 23870.		
KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
OS	Arabidopsis thaliana.		
PN	EPI033405-A2.		
PD	06-SEP-2000.		
PF	25-FEB-2000; 2000EP-0301439.		
XX	25-FEB-1999; 99US-0121825.		
PR	05-MAR-1999; 99US-0123180.		
PR	09-MAR-1999; 99US-0123548.		
PR	23-MAR-1999; 99US-0125788.		
PR	25-MAR-1999; 99US-0126284.		
PR	29-MAR-1999; 99US-0126785.		
PR	01-APR-1999; 99US-0127462.		
PR	06-APR-1999; 99US-0128234.		
PR	08-APR-1999; 99US-0128714.		
PR	16-APR-1999; 99US-0129845.		
PR	19-APR-1999; 99US-0130077.		
PR	21-APR-1999; 99US-0130449.		
PR	23-APR-1999; 99US-0130510.		
PR	23-APR-1999; 99US-0130891.		
PR	28-APR-1999; 99US-0131449.		
PR	30-APR-1999; 99US-0132048.		
PR	04-MAY-1999; 99US-0132407.		
PR	05-MAY-1999; 99US-0132484.		
PR	06-MAY-1999; 99US-0132485.		
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PR	07-MAY-1999; 99US-0132863.		
PR	11-MAY-1999; 99US-0134256.		
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PR	18-MAY-1999; 99US-0134768.		
PR	19-MAY-1999; 99US-0134941.		
PR	20-MAY-1999; 99US-0135124.		
PR	21-MAY-1999; 99US-0135353.		
PR	21-MAY-1999; 99US-0135629.		
PR	24-MAY-1999; 99US-0136021.		
PR	25-MAY-1999; 99US-0136392.		
PR	27-MAY-1999; 99US-0136782.		
PR	01-JUN-1999; 99US-0137222.		
PR	03-JUN-1999; 99US-0137528.		
PR	04-JUN-1999; 99US-0137502.		
PR	07-JUN-1999; 99US-0137724.		
PR	08-JUN-1999; 99US-0138094.		
PR	10-JUN-1999; 99US-0138540.		
PR	10-JUN-1999; 99US-0138847.		
PR	14-JUN-1999; 99US-0139119.		
PR	16-JUN-1999; 99US-0139452.		
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PR	18-JUN-1999; 99US-0139460.		
PR	18-JUN-1999; 99US-0139461.		
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PR	18-JUN-1999; 99US-0139463.		
PR	18-JUN-1999; 99US-0139750.		
PR	18-JUN-1999; 99US-0139763.		
PR	21-JUN-1999; 99US-0139817.		
PR	22-JUN-1999; 99US-0139899.		
PR	23-JUN-1999; 99US-0140353.		
PR	23-JUN-1		

PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
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PR 04-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
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PR 06-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147935.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
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PR 16-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
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PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
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PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
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PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
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PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161922.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.  
  
Query Match 55.4%; Score 1710; DB 21; Length 589;  
Best Local Similarity 55.1%; Pred. No. 8.6e-163;  
Matches 318; Conservative 107; Mismatches 146; Indels 6; Gaps 4;  
  
QY 5 LLLLLLPRTRADEHEHTYODKEEVVLWMNTVGPYHNROETYYKFSI.PFCVGGSKKSTISHVH 64  
Db 14 LLSVLLTPTTFASDSHKYQAEQVTLWNKVGYPNPNQETYYNYSLPFCRPSGNV-HKW 72  
  
QY 65 ETLGEALQGVLEFSGLDIKFKDDVMPATYCEIDLDKCKRDAFYVAIKNHYWQYVIDL 124  
Db 73 GGLGEVLGGNELIDSEIAIKFMKNVRSVICPLEDEAKVKHFKDAIESSYWFEEFMDL 132  
  
QY 125 PIWGIVGE--ADENGED--YLLWTKYKLEIGNGRNIVDNLTSSEKVKLVNTKIOMSY 180  
Db 133 SLWGFVGGELHPDKNSGKHVLYTHKNIVVYKNDQIIHVNLTQDNPRPLEAGKKMDLTY 192  
  
QY 181 SVKWKSDVKFEDRFDKYLDPSFFOHRTHWFSIENFMMVIELVGLVSLMRLTKDYA 240  
Db 193 SVQWIPNTVTFARRFDVLDYDPFHEQHWFISFNMVIFLTGLVSLMRLTRNDYA 252  
  
QY 241 RYSKE-EEMDDMDRLGDGEYKQVHGVDFRPSSHLIFSSSLIGSGCQFAVSLIIVA 299  
Db 253 KYAREDDLESLESDVSESGWKLVHGVDFRPASSLVLLSAVVGTAQALLVLLVILMA 312  
  
QY 300 MIEDLYTERGSMSTAIFVYAATSPVNGYFGSLYAROGGRWIKOMFIGAFIIPAMVCG 359  
Db 313 IVGTLYVGRGAIVTTFIVCYALTSEVSGYSGMYSRSGGKHVKCMVLTASLFLPCLFG 372  
  
QY 360 TAFINFIAIYHASKRAIPFGTMVAVCCICFVILPLNLVGLILGNLSGONFPCRYNA 419  
Db 373 IGFLNTAIFYGSLAAIPFGTMVVVFWGFIPLALLGTVVGGRNWSGAPNFCRVKT 432  
  
QY 420 VPRPIPEKKWFMEPAVIVCLGILPFGSIFTEMYPFTSFNAYKIYVYVGMMLVLVILC 479  
Db 433 IPRPIPEKKWVLTSPVSLMGLLPFGSIFTEMYPFTSFNAYKIYVYVGMMLVFLVILV 492  
  
QY 480 IVTVCTIVCTYFLLNAEDYRWQWTSFLSAASTAIYVYVYVYVYVYVYVYVYVYVYVYV 539  
Db 493 IVTVCTIVCTYFLLNAEDYRWQWTSFLSAASTAIYVYVYVYVYVYVYVYVYVYVYVYV 552  
  
QY 540 FGYMAVFSTALCMGATCYMCTSAFVBKIYTNVKID 576  
Db 553 FGYTMFCLGLGILCCAVGYLGSNLFVRRYRNKCD 589  
  
RESULT 13  
AAG21344  
ID AAG21344 standard; Protein; 608 AA.  
XX AAG21344;  
XX  
DT 17-Oct-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 23869.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX 06-SEP-2000.  
XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
XX 09-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
XX 16-APR-1999; 99US-0129845.  
XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
XX 23-APR-1999; 99US-0130510.  
XX 28-APR-1999; 99US-0130891.  
XX 30-APR-1999; 99US-0131449.  
XX 30-APR-1999; 99US-0132048.  
XX 04-MAY-1999; 99US-0132407.  
XX 05-MAY-1999; 99US-0132484.  
XX 06-MAY-1999; 99US-0132485.  
XX 06-MAY-1999; 99US-0132486.  
XX 07-MAY-1999; 99US-0132863.  
XX 11-MAY-1999; 99US-0134256.  
XX 14-MAY-1999; 99US-0134218.  
XX 14-MAY-1999; 99US-0134219.  
XX 14-MAY-1999; 99US-0134221.  
XX 18-MAY-1999; 99US-0134370.  
XX 19-MAY-1999; 99US-0134768.  
XX 20-MAY-1999; 99US-0134941.  
XX 21-MAY-1999; 99US-0135124.  
XX 24-MAY-1999; 99US-0135353.  
XX 25-MAY-1999; 99US-0135629.  
XX 27-MAY-1999; 99US-0136021.  
XX 28-MAY-1999; 99US-0136392.  
XX 01-JUN-1999; 99US-0136782.  
XX 03-JUN-1999; 99US-0137222.  
XX 04-JUN-1999; 99US-0137528.  
XX 07-JUN-1999; 99US-0137502.  
XX 08-JUN-1999; 99US-0137724.  
XX 10-JUN-1999; 99US-0138094.  
XX 10-JUN-1999; 99US-0138540.  
XX 14-JUN-1999; 99US-0138847.  
XX 16-JUN-1999; 99US-0139119.  
XX 16-JUN-1999; 99US-0139452.  
XX 17-JUN-1999; 99US-0139453.  
XX 18-JUN-1999; 99US-0139492.  
XX 18-JUN-1999; 99US-0139454.  
XX 18-JUN-1999; 99US-0139455.  
XX 18-JUN-1999; 99US-0139456.  
XX 18-JUN-1999; 99US-0139457.  
XX 18-JUN-1999; 99US-0139458.  
XX 18-JUN-1999; 99US-0139459.  
XX 18-JUN-1999; 99US-0139460.  
XX 18-JUN-1999; 99US-0139461.  
XX 18-JUN-1999; 99US-0139462.  
XX 18-JUN-1999; 99US-0139463.  
XX 18-JUN-1999; 99US-0139750.  
XX 18-JUN-1999; 99US-0139763.  
XX 21-JUN-1999; 99US-0139817.  
XX 22-JUN-1999; 99US-0139899.  
XX 23-JUN-1999; 99US-0140353.  
XX 23-JUN-1999; 99US-0140354.  
XX 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
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08-OCT-1999;	99US-0158232.				
12-OCT-1999;	99US-0158369.				
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QY	420	VPRPIPEKKWFMEPAVITCVLGGLPFGSIFPTIEMFYFIETSFWAYKIYVYGFMMLVLVILC	479
Db	452	IPRPIPEKKWLTFSVSLMGGLLPFGSIFTIEMFYFVTSEWNKIVYVYGFMLLVFVLV	511
QY	480	IIVTCVTTICTYTFLLNAEDYRWQWTSLSAASTAIYVMYSFYVYFFKTKMYGLFQTSPY	539
Db	512	IIVTCVTVIGTYFELLNAENYHQWTSFESAATAVYVLYSLIYVYVKTKMSGFFQTSEY	571
QY	540	FGYMAVFSTALGMCAGIYMGTSFAFRKRIYTNVKID	576
Db	572	FGYTMFCLGILCGAVGYLGSNFLVRRIYRNICKD	608
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XX	DT	18-OCT-2000 (first entry)	
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 57321.	
KW	Protein identification;	signal transduction pathway; metabolic pathway;	
KW	hybridisation assay;	genetic mapping; gene expression control; promoter;	
KW	termination sequence.		
OS	Arabidopsis thaliana.		
XX	EP1033405-A2.		
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XX	PF	25-FEB-2000; 2000EP-0301439.	
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Best Local Similarity 54.4%; Pred. No. 1.1e-158;  
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DB 14 LLVSLTPTTFASDSDBKHQABEQVTLWNVKVPYNNQETNYSLPFCRPSGNNV-HKW 72

QY 65 ETLEALOGVELEPSGLDIKFKDQVMPATYCEIDLDDKRDQAFVYAIKNHXYQWYIDDL 124  
DB 73 GGLGVGGLNELIDSEIAIKMKNVRSVVICPLEDEAKVHKHFKDAIESWFEFFM--- 129

QY 125 PIWGTIVGE--ADENGED--YVLWTYKKLEIGFNGNRIVDVNLTSSEKVKLVNPKIQMSY 180  
DB 130 ---GPGVGLHPDKNSEKCHVLYTHKNVVKYKNDQIIHVNLTQDNPRPLEAGKKMDLTY 186

QY 181 SVKWKSDVKFEDRPDKYLDSPFOHRTHWFSIFNSFMVIFLVGLVSMILMRLTRKDYA 240  
DB 187 SVQWITPTNVTFARRFDVLYDPFPEHQIHWFSIFNSFMVIFLVGLVSMILMRLTRNDYA 246

QY 241 RYSKE-EEMDDMDRLDGEYQKQVHGDFRPSHPLIFSSILGSGCOIFAVSLIIVIA 299  
DB 247 KYAREDDLESRLERDVSESGKLVHGDFRPASSVLVLSAVGTGAOLALLVLLVILMA 306

QY 300 MIEDLYTERGSMLETAIFVYAATSPVNGYFGGSLYAROGGRWIKQMFIGAFLIPAMVCG 359  
DB 307 IVGTLVGRGAIVTTFIVCYALTSPVSGYVSGMGYSRSGGKHWIKCMVLTASLPFLCFG 366

QY 360 TAFFINFTAIYHASRAIPFGTMVAVCCICFVILPLNLVTILGRNLUSGQPNFPCRVNA 419  
DB 367 IGFLNTTAIFYGSLAIPFGTMVAVFVIMGFISFPLALLGTVVGRNWSGAPNRCRVKT 426

QY 420 VPRPTPEKKWMEPAVIVCLGSLPFGSIFTEMVFIFTSFWAYKIYVYVGFMLVLVILC 479  
DB 427 IPRPIPEKKWYLTSPVSLMGLLPFGSIFTEMVFVFTSFWNKYVYVYVGFMLLVFVILV 486

QY 480 IVTCVTIVCTYFLLNAEDYRWQMTSFLSAASTAIYVYVYVYVYVYVYVYVYVYVYVY 539  
DB 487 IVTCVTIVCTYFLLNAENYHWQMTSFFSAASTAVYVYVYVYVYVYVYVYVYVYVYV 546

QY 540 FGYMAVFTALGIMCGAIGYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVYVY 576  
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RESULT 15  
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XX AC AAG45637;  
XX DT 18-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 57320.  
XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX NW hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
XX PR 05-MAR-1999; 99US-0123180.  
XX PR 09-MAR-1999; 99US-0123548.  
XX PR 23-MAR-1999; 99US-0125788.  
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PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
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